

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1617	74.2	1617	6	QX0505714	Sequence
2	1617	74.2	1617	6	AX5065544	QX0506544 Sequence
3	1615.8	74.2	1619	8	AF056190	AF056190 Arabidops
4	1614	74.1	1614	8	AF106334	AF106334 Arabidops
5	1610.6	73.9	1617	8	AF685183	AF685183 Arabidops
6	1610.6	73.9	1617	8	AF510074	AF510074 Arabidops
7	1180	54.2	1723	8	AF189676	AF189676 Brassica
8	1141.8	52.4	1641	8	AF490586	AF490586 Arabidops
9	889.6	40.8	2135	8	AY028416	AY028416 Citrus x
10	889.4	40.8	2485	8	AF515632	AF515632 Gossypium
11	858	39.4	1752	8	AY513732	AY513732 Medicago
12	858	39.4	2232	8	AY456096	AY456096 Medicago
13	833.4	38.3	1656	8	AY371319	AY371319 Chenopodi
14	832.8	38.2	1668	6	E63046	E63046 Na+/H+ anti
15	832.8	38.2	1668	6	E63047	E63047 Na+/H+ anti
16	832.8	38.2	2637	8	AB038492	AB038492 Atriplex
17	826.4	37.9	2668	8	AY131235	AY131235 Salicornia
18	821.6	37.7	1668	8	AY211397	AY211397 Atriplex
19	821.2	37.7	2553	6	BD012815	BD012815 Gene codi

Db 181 GTTACCAATTTTGTGATTAGTAAAGGAAAAAGCTCGCATCTTCTCGTCTTTTAGTAGAAT 240
Qy 526 CTTTCTTTCATATATCTTTTGGCACCCCATATATTAATCAATGCAAGGTTTCAAGTAAAAAG 585
Db 241 CTTTCTTTCATATATCTTTTGGCACCCCATATATTAATCAATGCAAGGTTTCAAGTAAAAAG 300
Qy 586 AAGCAGTTTTTCCGCAATTTCTGACTATATATGCTTTTTTGGTGCTGTTGGGACTATATT 645
Db 301 AAGCAGTTTTTCCGCAATTTCTGACTATATATGCTTTTTTGGTGCTGTTGGGACTATATT 360
Qy 646 TCTTGCAATCATATCTCTAGGTGTAAACACAGTTCTTTTAAAGAGTTGCAATTTGGAACC 705
Db 361 TCTTGCAATCATATCTCTAGGTGTAAACACAGTTCTTTTAAAGAGTTGCAATTTGGAACC 420
Qy 706 TTTGACTGGGTGATATCTTGCTATTTGGTGCCATATTTGCTGCAACAGATTCAAGTATGT 765
Db 421 TTTGACTGGGTGATATCTTGCTATTTGGTGCCATATTTGCTGCAACAGATTCAAGTATGT 480
Qy 766 ACACCTGCAGTTCTGAACTCAAGACGAGACACCTTTTGTCTTTACAGTCTTTGATTCGGAGAG 825
Db 481 ACACCTGCAGTTCTGAACTCAAGACGAGACACCTTTTGTCTTTACAGTCTTTGATTCGGAGAG 540
Qy 826 GGTGTGTGAATGATGCAACGT CAGTTGTGTCTTTCAACGGCAATTCAGAGCTTTGATCTC 885
Db 541 GGTGTGTGAATGATGCAACGT CAGTTGTGTCTTTCAACGGCAATTCAGAGCTTTGATCTC 600
Qy 886 ACTCAGCTTAAACAGAGCTCTTTTCACTCTTTTGGAACTCTTCTGATTTTGTCTC 945
Db 601 ACTCAGCTTAAACAGAGCTCTTTTCACTCTTTTGGAACTCTTCTGATTTTGTCTC 660
Qy 946 CTAAGTACCTCTGTTGCTGCTCAACCGCTCTGATAAGTGCATGCTTATCAAGAAGCTA 1005
Db 661 CTAAGTACCTCTGTTGCTGCTCAACCGCTCTGATAAGTGCATGCTTATCAAGAAGCTA 720
Qy 1005 TACTTTGGAAGCACTCAACTGACCGAGAGGTGTGCCCTTATGATGCTTATGCGGTATCTT 1065
Db 721 TACTTTGGAAGCACTCAACTGACCGAGAGGTGTGCCCTTATGATGCTTATGCGGTATCTT 780
Qy 1066 TCTTATATGCTTGAGCTTTTTCGACTTGAGCGGTATCTTCACTGCTGTTTCTGCTGCT 1125
Db 781 TCTTATATGCTTGAGCTTTTTCGACTTGAGCGGTATCTTCACTGCTGTTTCTGCTGCT 840
Qy 1126 ATTTGTATGCTGCCATTTACATATGCGACATGTAACGGAGAGCTCAAGAATTAACACAAG 1185
Db 841 ATTTGTATGCTGCCATTTACATATGCGACATGTAACGGAGAGCTCAAGAATTAACACAAG 900
Qy 1186 CATACCTTTGCAACTTTGTCAATTTCTTGGGAGACATTTATTTCTTGTATGTTGGAATG 1245
Db 901 CATACCTTTGCAACTTTGTCAATTTCTTGGGAGACATTTATTTCTTGTATGTTGGAATG 960
Qy 1246 GATGCTTTGGACATTTGACAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA 1305
Db 961 GATGCTTTGGACATTTGACAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA 1020
Qy 1306 GTGAGCTCAATCTTAATGGTCTGTCTATGTTGGAAGGACGCTGCTCTTTCCGTTA 1365
Db 1021 GTGAGCTCAATCTTAATGGTCTGTCTATGTTGGAAGGACGCTGCTCTTTCCGTTA 1080
Qy 1366 TCGTTTCTATCTAATCTTACGCAAGAGAAATCAAGCGAGAAATCAACTTTAAACATGAG 1425
Db 1081 TCGTTTCTATCTAATCTTACGCAAGAGAAATCAAGCGAGAAATCAACTTTAAACATGAG 1140
Qy 1426 GTTGTGATTTGGTCTGGTCTCATGAGAGTGTCTGATATCTATGCTCTTTGCAATCAAC 1485
Db 1141 GTTGTGATTTGGTCTGGTCTCATGAGAGTGTCTGATATCTATGCTCTTTGCAATCAAC 1200
Qy 1486 AAGTTTACAAAGGCGGGCACACAGATGTACGCGGAAATGCAATCATGATCAAGAGTACG 1545
Db 1201 AAGTTTACAAAGGCGGGCACACAGATGTACGCGGAAATGCAATCATGATCAAGAGTACG 1260
Qy 1546 ATAACTGTCTGCTTTTATAGCA CAGTGGTGTGTTGTTGCTGACCAACCACTCATAGC 1605
Db 1261 ATAACTGTCTGCTTTTATAGCA CAGTGGTGTGTTGTTGCTGACCAACCACTCATAGC 1320

Qy 1606 TACCTATTACCGACCAAGAGCCACACGAGCATGTTATCTGATGACAAACCCCAAAA 1665
Db 1321 TACCTATTACCGACCAAGAGCCACACGAGCATGTTATCTGATGACAAACCCCAAAA 1380
Qy 1666 TCCATACATATCCCTTTTGGACCAAGACTCGTTTCATTAGAGCTTTCAGGGAACCACAAT 1725
Db 1381 TCCATACATATCCCTTTTGGACCAAGACTCGTTTCATTAGAGCTTTCAGGGAACCACAAT 1440
Qy 1726 GTGCTCTGGCTGACAGTATACGTGGCTTTTGACACGGCCCACTTCGAACCGTGCATTAC 1785
Db 1441 GTGCTCTGGCTGACAGTATACGTGGCTTTTGACACGGCCCACTTCGAACCGTGCATTAC 1500
Qy 1786 TACTGGAGACAATTTGATGACTCTTTCATGCGACCGCTTTCATGAGGTCGTGGCTTTGTA 1845
Db 1501 TACTGGAGACAATTTGATGACTCTTTCATGCGACCGCTTTCATGAGGTCGTGGCTTTGTA 1560
Qy 1846 CCCTTTGTTCCAGGTTCTTCCAACTGAGAGAAACCTCTCTGATCTTTAGTAAGGCTTGA 1902
Db 1561 CCCTTTGTTCCAGGTTCTTCCAACTGAGAGAAACCTCTCTGATCTTAGTAAGGCTTGA 1617

RESULT 2
AX506544
LOCUS AX506544 1617 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 1239 from Patent WO0216655.
ACCESSION AX506544
VERSION AX506544.1 GI:23387781
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopses.
1
Harper, J. P., Kreps, J., Wang, X. and Zhu, T.
Stress-regulated genes of plants, transgenic plants containing
same, and methods of use
Patent: WO 0216655-A 1239 28-FEB-2002;
The Scripps Research Institute (US) ; Syngenta Participations AG
(CH)
FEATURES
Location/Qualifiers
source 1..1617
/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"

Query Match 74.2%; Score 1617; DB 6; Length 1617;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1617; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 286 ATGTTGGATTTCTTAGTGTGAAACTGCTTCGTTATCGACATCTGATCAGCTTCTGTG 345
Db 1 ATGTTGGATTTCTTAGTGTGAAACTGCTTCGTTATCGACATCTGATCAGCTTCTGTG 60
Qy 346 GTTGGTTGAATCTCTTTTGGACATCTTCTTGTGCTGTATGTTCTTGTGTCATCTTTG 405
Db 61 GTTGGTTGAATCTCTTTTGGACATCTTCTTGTGCTGTATGTTCTTGTGTCATCTTTG 120
Qy 406 GAAGAGATAGATCGATGAAACGAAATCCATCACCCCTTGTGATTTGGGCTAGGCACTGGT 465
Db 121 GAAGAGATAGATCGATGAAACGAAATCCATCACCCCTTGTGATTTGGGCTAGGCACTGGT 180
Qy 466 GTTACCAATTTTGTGATTAGTAAAGGAAAGCTCGCATCTTCTCGCTTTTGTAGTGAAGAT 525
Db 181 GTTACCAATTTTGTGATTAGTAAAGGAAAGCTCGCATCTTCTCGCTTTTGTAGTGAAGAT 240
Qy 526 CTTTCTTTCATATATCTTTTGGCCACCCCATTAATATTCATGCAAGGTTTCAAGTAAAAAG 585
Db 241 CTTTCTTTCATATATCTTTTGGCCACCCCATTAATATTCATGCAAGGTTTCAAGTAAAAAG 300
Qy 586 AAGCAGTTTTTCCGCAATTTTCGTGACTATTTATGCTTTTTTGTGCTGTTTGTGGGACTATTATT 645

Db 301 AAGCAGTTTTCGCAATTCGAGACTATTATGCTTTTGGTGTGTGCGACTATTATT 360
Qy 646 TCTTGACAAATCATATCTCTAGGTGTAACAACAGTCTCTTTAAGAAGTTGGACATTTGAACC 705
Db 361 TCTTGACAAATCATATCTCTAGGTGTAACAACAGTCTCTTTAAGAAGTTGGACATTTGAACC 420
Qy 706 TTTGACTCGGTGATTATCTTGCTATTGTTGTCATATTTGCTGCAACAGATTCAATGATGT 765
Db 421 TTTGACTCGGTGATTATCTTGCTATTGTTGTCATATTTGCTGCAACAGATTCAATGATGT 480
Qy 766 ACAGTCAGGTTCTGAATCAAGACGAGACACCTTTGCTTTACAGTCTGCTATTTCGGAGAG 825
Db 481 ACAGTCAGGTTCTGAATCAAGACGAGACACCTTTGCTTTACAGTCTGCTATTTCGGAGAG 540
Qy 826 GGTGTTGTGAATGATCAACAGTCAGTGTGTGCTCTCAACGCGATTTCAGAGCTTTGATCTC 885
Db 541 GGTGTTGTGAATGATCAACAGTCAGTGTGTGCTCTCAACGCGATTTCAGAGCTTTGATCTC 600
Qy 886 ACTACCTAAACACGAAAGTCTTTTCACTCTCTTGGAACTCTTTGTAATTTGTTTCTC 945
Db 601 ACTACCTAAACACGAAAGTCTTTTCACTCTCTTGGAACTCTTTGTAATTTGTTTCTC 660
Qy 946 CTAAGTACCTTGTGTTGCTGCAACCGCTCTGATAAGTGCATATGTTATCAAGAAGCTA 1005
Db 661 CTAAGTACCTTGTGTTGCTGCAACCGCTCTGATAAGTGCATATGTTATCAAGAAGCTA 720
Qy 1006 TACTTTGGAAGGCACCTCAACTGACGAGAGGTTGCCCTTATCATGCTTATGCGGTATCTT 1065
Db 721 TACTTTGGAAGGCACCTCAACTGACGAGAGGTTGCCCTTATCATGCTTATGCGGTATCTT 780
Qy 1066 TCTTATATGCTGCTGAGCTTTTCGACTTTGAGCGGTATCCTCACTGTGTTTTCTGTGT 1125
Db 781 TCTTATATGCTGCTGAGCTTTTCGACTTTGAGCGGTATCCTCACTGTGTTTTCTGTGT 840
Qy 1126 ATTGTGATGCTCCATTAACATGCGACATGTAACGAGAGCTCAAGATTAACAACAAG 1185
Db 841 ATTGTGATGCTCCATTAACATGCGACATGTAACGAGAGCTCAAGATTAACAACAAG 900
Qy 1186 CATACCTTTGCAACTTTGCTATTTCTTGGGAGACATTTATTTCTTGTATGCTGGAATG 1245
Db 901 CATACCTTTGCAACTTTGCTATTTCTTGGGAGACATTTATTTCTTGTATGCTGGAATG 960
Qy 1246 GATGCTTTGGAATGACATGGAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA 1305
Db 961 GATGCTTTGGAATGACATGGAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA 1020
Qy 1306 GTGAGTCAATCCTAAATGCGTCTGCTGATGTTGGAAGAGAGCGTTCGTTCCGTTA 1365
Db 1021 GTGAGTCAATCCTAAATGCGTCTGCTGATGTTGGAAGAGAGCGTTCGTTCCGTTA 1080
Qy 1366 TCGTTTCTATCTAACTTAGCCAAAGAAATCAAGCGAGAAATCAACTTTAAACATGCAG 1425
Db 1081 TCGTTTCTATCTAACTTAGCCAAAGAAATCAAGCGAGAAATCAACTTTAAACATGCAG 1140
Qy 1426 GTTGTGATTTGGTGTCTGCTCATGAGAGGTGCTGTATCTATGCTCTTCGATACAAC 1485
Db 1141 GTTGTGATTTGGTGTCTGCTCATGAGAGGTGCTGTATCTATGCTCTTCGATACAAC 1200
Qy 1486 AAGTTTACAGGCGCGGACACAGATGTACCGGGAATGCAATCATGATCAAGATGAG 1545
Db 1201 AAGTTTACAGGCGCGGACACAGATGTACCGGGAATGCAATCATGATCAAGATGAG 1260
Qy 1546 ATAACCTGCTGCTTTTATGACAGTGTGTTTGTGATGCTGACCAACCACTCATATAGC 1605
Db 1261 ATAACCTGCTGCTTTTATGACAGTGTGTTTGTGATGCTGACCAACCACTCATATAGC 1320
Qy 1605 TACCTATTACCGCACGCAACCGCACAGCATGTTATCTGATGACAAACCCCAAAA 1665
Db 1321 TACCTATTACCGCACGCAACCGCACAGCATGTTATCTGATGACAAACCCCAAAA 1380
Qy 1666 TCCATACATATCCCTTTGTTGACCAAGACTCGTTTCATTGAGCCTTCAGGGAACCAAT 1725

Db 1381 TCCATACATATCCCTTTGTTGGACCAAGACTCGTTTCATTGAGCCTTCAGGGAACCAACAAT 1440
Qy 1726 GTGCCCTCGCCCTGACAGTATACGTGGCTTTCTTGACACGCGCCCACTCGAACCGTGCATTAC 1785
Db 1441 GTGCCCTCGCCCTGACAGTATACGTGGCTTTCTTGACACGCGCCCACTCGAACCGTGCATTAC 1500
Qy 1786 TACTCGAGACAATTTGATGACTCTCTTCATGCGACCCGCTTTTGGAGGTGCTGGCTTTGTA 1845
Db 1501 TACTCGAGACAATTTGATGACTCTCTTCATGCGACCCGCTTTTGGAGGTGCTGGCTTTGTA 1560
Qy 1846 CCCTTTGTTCCAGGTTCTCCAACTGAGAGAACCTCTCGATCTTAGTAAGGCTTGA 1902
Db 1561 CCCTTTGTTCCAGGTTCTCCAACTGAGAGAACCTCTCGATCTTAGTAAGGCTTGA 1617

RESULT 3
AF056190
LOCUS AF056190 1619 bp mRNA linear PLN 06-JUN-2000
DEFINITION Arabidopsis thaliana Na+/H+ exchanger (NHX1) mRNA, complete cds.
ACCESSION AF056190
VERSION AF056190.1 GI:6650176
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 1619)
AUTHORS Quintero, F.J., Blatt, M.R. and Pardo, J.M.
TITLE Functional conservation between yeast and plant endosomal Na(+)/H(+) antiporters
JOURNAL FEBS Lett. 471 (2-3), 224-228 (2000)
MEDLINE 20231718
PUBMED 10767428
REFERENCE 2 (bases 1 to 1619)
AUTHORS Quintero, F.J.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-1998) Biologia Vegetal, IRNASE (CSIC), Avda. Reina Mercedes s/n, Sevilla 41012, Spain
FEATURES
source
1..1619
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
gene
1..1619
/gene="NHX1"
CDS
3..1619
/gene="NHX1"
/note="Na+/H+ antiporter"
/codon_start=1
/product="Na+/H+ exchanger"
/protein_id="AAF21755.1"
/db_xref="GI:6650177"
/translation="MDSLVSKPLSLSDSHASVVALNLFVALLCACIVLGHLEENR
WMNSITALLIGLGTITLISIKGSHLLVFSDELFFIYLLPIIFNAQFQVKKKQ
FFRNFVIMLFAGVGTIIISLTIGVTFPKDIDIGTDLGDIAGIAIFAATDSVC
TLQVNDDETPLYSLVFGGVNDATSVVFNAIQSPDLTHLNHEAAPHLLGNFLYL
FLICLLGAATGLISAVVIKKLYFRHSTDRVALMMLAVLSYMLASLFDLSGLITV
PFCIVMSHYTHNVNTESSRITTKHTFATLSFLAETFLFYVGHDAIDIKRVSVD
PGTSIAVSSILMLGLVMVRAAFVPLSFLSNLAKNQSEKINFNQVVIWWSGLMRGA
VSMALANYKTRAGHTDVRGNAMITSTITVCLFSTVVFGLTKPLISYLLPHQNAIT
SMLSDNTPKSIHIFLLDQDSIFBPSGNHNVPRDPSIRGFLTRPTRTVHYVWRQDDDS
FMRPVFGRGVFPVPGSPTEPNPDLSKA"

ORIGIN
Query Match 74.2%; Score 1615.8; DB 8; Length 1619;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1617; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 284 CAATGTTGGATCTCTAGTGTGGAACCTGCTTGGTTATCGACATCTGATCAGCTTCTG 343
Db 1 CAATGTTGGATCTCTAGTGTGGAACCTGCTTGGTTATCGACATCTGATCAGCTTCTG 60

QY 344 TGGTGGCTGGAATCTCTTTGTTGCACTCTTTTGTGCTGTATGTTCTTGGTCACTTT 403
Db |||
61 TGGTGGCTGGAATCTCTTTGTTGCACTCTTTTGTGCTGTATGTTCTTGGTCACTTT 120
QY 404 TGAAGAGAAATAGATGGAATGAACGAATCCATCACCGCTTGTGATTTGGCTAGGCACTG 463
Db |||
121 TGAAGAGAAATAGATGGAATGAACGAATCCATCACCGCTTGTGATTTGGCTAGGCACTG 180
QY 464 GTGTTACCACTTTGTTGATTAGTAAGGAAGAAAGCTCGCATCTTCTCGTCTTTAGTGAAG 523
Db |||
181 GTGTTACCACTTTGTTGATTAGTAAGGAAGAAAGCTCGCATCTTCTCGTCTTTAGTGAAG 240
QY 524 ATCTTTTCTTCATATATCTTTTGGCACCCATTATATCAATGCGAGGTTTCAAGTAAAAA 583
Db |||
241 ATCTTTTCTTCATATATCTTTTGGCACCCATTATATCAATGCGAGGTTTCAAGTAAAAA 300
QY 584 AGAAGCAGTTTTTCCGCAATTTCTGTAATATTATGCTTTTGGTGTCTGTGGGACTATTA 643
Db |||
301 AGAAGCAGTTTTTCCGCAATTTCTGTAATATTATGCTTTTGGTGTCTGTGGGACTATTA 360
QY 644 TTTCTTGCACAATCATATCTCTAGGTGTAACACAGTTCTTTAAGAGTTGGACATGGAA 703
Db |||
361 TTTCTTGCACAATCATATCTCTAGGTGTAACACAGTTCTTTAAGAGTTGGACATGGAA 420
QY 704 CCTTTGACTGGGTGATTATCTTGTATTGGTGCCATATTTGCTGCAACAGATTCAAGTAT 763
Db |||
421 CCTTTGACTGGGTGATTATCTTGTATTGGTGCCATATTTGCTGCAACAGATTCAAGTAT 480
QY 764 GTAACATGAGTTCTGAATCAAGACGAGACACCTTTGCTTTPACAGTCTTGTATTGGTTC 823
Db |||
481 GTAACATGAGTTCTGAATCAAGACGAGACACCTTTGCTTTPACAGTCTTGTATTGGTTC 540
QY 824 AGGTTGTTGTAATGATGCAAGCTCAGTTGCTGCTTCAACCGGATTCAGAGCTTTGATC 883
Db |||
541 AGGTTGTTGTAATGATGCAAGCTCAGTTGCTGCTTCAACCGGATTCAGAGCTTTGATC 600
QY 884 TCACCTCACCTAAACCAAGAGCTGCTTTTCATCTTCTTGGAACTTCTTGTATTGGTTC 943
Db |||
601 TCACCTCACCTAAACCAAGAGCTGCTTTTCATCTTCTTGGAACTTCTTGTATTGGTTC 660
QY 944 TCCTAAGTACCTTGTGCTGCTCAACCGGCTTGATAAGTGCATGTTATCAAGAAAGC 1003
Db |||
661 TCCTAAGTACCTTGTGCTGCTCAACCGGCTTGATAAGTGCATGTTATCAAGAAAGC 720
QY 1004 TATACCTTGGAGGCACTCAACTGACCGAGAGTTGCCCTTATGATGTTATGGGCTATC 1063
Db |||
721 TATACCTTGGAGGCACTCAACTGACCGAGAGTTGCCCTTATGATGTTATGGGCTATC 780
QY 1064 TTTCTTATATGCTTGTGAGCTTTTCGACTTCAGCGGTATCCTCACTGTGTTTTTCTGTG 1123
Db |||
781 TTTCTTATATGCTTGTGAGCTTTTCGACTTCAGCGGTATCCTCACTGTGTTTTTCTGTG 840
QY 1124 GTATTGTGATGCCATTACATGCGCACAATGTAAACGAGAGCTCAAGAAATAACAA 1183
Db |||
841 GTATTGTGATGCCATTACATGCGCACAATGTAAACGAGAGCTCAAGAAATAACAA 900
QY 1184 AGCATACCTTTCGAACCTTTGCTTTCGCGGACATTTATTTTCTGTATGTTGAA 1243
Db |||
901 AGCATACCTTTCGAACCTTTGCTTTCGCGGACATTTATTTTCTGTATGTTGAA 960
QY 1244 TGGATGCTTGGACATTGACAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCG 1303
Db |||
961 TGGATGCTTGGACATTGACAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCG 1020
QY 1304 CAGTGAGCTCAATCTTAATGGGTCTGGTCAATGGTTTGGAGAGCAGCGTTTCGTCTTCGGT 1363
Db |||
1021 CAGTGAGCTCAATCTTAATGGGTCTGGTCAATGGTTTGGAGAGCAGCGTTTCGTCTTCGGT 1080
QY 1364 TATCGTTCTTATCTTAACCTTAGCCAGAGAAATCAAGCGAGAAATCACTTTAATATGC 1423
Db |||
1081 TATCGTTCTTATCTTAACCTTAGCCAGAGAAATCAAGCGAGAAATCACTTTAATATGC 1140
QY 1424 AGGTTGTGATTTGGTGGTCTGGTCTCATGAGAGGTGCTGTATCTATGGCTCTTGCATACA 1483

Db |||
1141 AGGTTGTGATTTGGTGGTCTGGTCTCATGAGAGTGCTGTATCTATGCTCTTGCATACA 1200
QY 1484 ACAAGTTTACAAGGGCCGGGCAACAGATGTACCGGGAATGCAATCATGATCAGAGTA 1543
Db |||
1201 ACAAGTTTACAAGGGCCGGGCAACAGATGTACCGGGAATGCAATCATGATCAGAGTA 1260
QY 1544 CGATAACCTGCTGCTTTTGTAGACAGTGGTGTGTTGTATGCTACCAAAACCATCTATAA 1603
Db |||
1261 CGATAACCTGCTGCTTTTGTAGACAGTGGTGTGTTGTATGCTACCAAAACCATCTATAA 1320
QY 1604 GCTACCTATTACCGCACAGAAACCGCACCGAGCATGTTATCTGTATGACAAACCCCAA 1663
Db |||
1321 GCTACCTATTACCGCACAGAAACCGCACCGAGCATGTTATCTGTATGACAAACCCCAA 1380
QY 1664 AATCAATACATATCCCTTTTGTGACCAAGACTCGTTCAATGAGCCTTCAGGGAACACA 1723
Db |||
1381 AATCAATACATATCCCTTTTGTGACCAAGACTCGTTCAATGAGCCTTCAGGGAACACA 1440
QY 1724 ATGTGCTCTCGGCTGACAGTATACGTGCTTCTTGAACGCGCCACTCGAACCGTCAAT 1783
Db |||
1441 ATGTGCTCTCGGCTGACAGTATACGTGCTTCTTGAACGCGCCACTCGAACCGTCAAT 1500
QY 1784 ACTACTGAGACAATTTGATGACTCTTTCATGCGACCGCTCTTTGGAGGTCGTGGCTTTG 1843
Db |||
1501 ACTACTGAGACAATTTGATGACTCTTTCATGCGACCGCTCTTTGGAGGTCGTGGCTTTG 1560
QY 1844 TACCTTTTGTTCAGGTTCTCCAACTGAGAGAAACCTCTCTGATCTTATGAGGCTTGA 1902
Db |||
1561 TACCTTTTGTTCAGGTTCTCCAACTGAGAGAAACCTCTCTGATCTTATGAGGCTTGA 1619
RESULT 4
AF106324
LOCUS
DEFINITION Arabidopsis thaliana sodium proton exchanger Nhx1 mRNA, partial cds.
ACCESSION AF106324
VERSION AF106324.1 GI:4324596
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 1614)
AUTHORS Gaxiola,R.A., Rao,R., Sherman,A., Grisafi,P., Alper,S.L. and Fink,G.R.
TITLE The Arabidopsis thaliana proton transporters, AtNhx1 and Avp1, can function in cation detoxification in yeast
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (4), 1480-1485 (1999)
MEDLINE 99145575
PUBMED 9990049
REFERENCE 2 (bases 1 to 1614)
AUTHORS Fink,G.R.
TITLE Direct Submission
JOURNAL Submitted (12-NOV-1998) Whitehead, Nine Cambridge Center, Cambridge, MA 02142, USA
FEATURES
source
1. 1614
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/cultivar="Columbia"
/db_xref="taxon:3702"
1. .>1614
/codon_start=1
/product="sodium proton exchanger Nhx1"
/protein_id="AADI6946.1"
/db_xref="GI:4324597"
translation="MLDSIVSKLPSLSTSDHASVVALNLFVALLCACTIVLGHLEENR
WMNESITALLIGLTVGTTILLISKSKSHLLVFSEDFLYLLPFIIFNAGFOYKQKQ
FFRNFVIMLPFAGVGTIISLTIIISLQVTPFKLIDITFDLGLDYLALGAIPAATDSVC

TLQVLDNDBTPLLISLVFGEGVNDATSVVFNALQSPDLTHLNHEAAPHLLGNFLYL
FLSLTLGAAATGLISAYIVIKLYFGRHSRDREVALMMLMAYLSYMLAELDFLSGLTV
PFCGIYMSHYTHNTVWTESSRITTKHTFATLSEFLAETFIPLYGMDALDIDKWRVSVD
PGTSIAVSSILMGLVMVGRAAFPVPLSLNAXKQSEKINFNMQVVIWWSGLMRGA
VSMALYNKFTRAHGTDRGNALMITSITIVCLFSTVVFGLMKPLISVLLPHONATT
SMLSDNTPKSHIPLLDODSFLPSGNHNVRPDSIRGFLRTPRTVHYWYRQFDDSD
FMRPVGGRGVFPVFGSPFERNPFDLSKA"

ORIGIN

Query Match 74.1%; Score 1614; DB 8; Length 1614;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1614; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	286	ATGTTGGATCTCTAGTGTGCGAACTGCGCTTGTATCGACATCTGATCACGCTTCTGTG	345
DB	1	ATGTTGGATCTCTAGTGTGCGAACTGCGCTTGTATCGACATCTGATCACGCTTCTGTG	60
QY	346	GTTCGCTTCAATCTCTTTCGACCTCTTTCGCTTGTATGTTCTTGGTCTATCTTTTG	405
DB	61	GTTCGCTTCAATCTCTTTCGACCTCTTTCGCTTGTATGTTCTTGGTCTATCTTTTG	120
QY	406	GAAGAGATAGATGATGAACCAATCCATCACCGCTTGTATGTTGGGCTAGGCACTGCT	465
DB	121	GAAGAGATAGATGATGAACCAATCCATCACCGCTTGTATGTTGGGCTAGGCACTGCT	180
QY	466	GTACCAATTTGTGATTAGTAAAGGAAAAAGCTCGCATCTTCTCGTCTTTAGTGAAGAT	525
DB	181	GTACCAATTTGTGATTAGTAAAGGAAAAAGCTCGCATCTTCTCGTCTTTAGTGAAGAT	240
QY	526	CTTTCTTCAATATCTTTTGGCAAGCAATATATCAATGCAAGGTTTCAAGTAAAAAG	585
DB	241	CTTTCTTCAATATCTTTTGGCAAGCAATATATCAATGCAAGGTTTCAAGTAAAAAG	300
QY	586	AAGCAGTTTTTCGCAATTTCTGACTATTATGCTTTTTTGGTGTGTTGGGCACTATT	645
DB	301	AAGCAGTTTTTCGCAATTTCTGACTATTATGCTTTTTTGGTGTGTTGGGCACTATT	360
QY	646	TCTTGCAATCATATCTCTAGTGTGAACAGATTTCTTTAAGAAGTTGGACATTTGAACC	705
DB	361	TCTTGCAATCATATCTCTAGTGTGAACAGATTTCTTTAAGAAGTTGGACATTTGAACC	420
QY	706	TTTGACTGGGTGATATCTTGTATGTGTCATATTTGTCGCAAGATTCAGTATGT	765
DB	421	TTTGACTGGGTGATATCTTGTATGTGTCATATTTGTCGCAAGATTCAGTATGT	480
QY	766	ACACTGCAGTTCTGAATCAAGCAGACACCTTTGCTTTTACAGTCTTGTATTCGAGAG	825
DB	481	ACACTGCAGTTCTGAATCAAGCAGACACCTTTGCTTTTACAGTCTTGTATTCGAGAG	540
QY	826	GGTGTGTGAATGATGCAACGTCAAGTTGTGCTCTTCAACCGCATTCAGAGCTTTGATCTC	885
DB	541	GGTGTGTGAATGATGCAACGTCAAGTTGTGCTCTTCAACCGCATTCAGAGCTTTGATCTC	600
QY	886	ACTACCTAAACAGCAAGCTGCTTTTCACTCTTCTTGGAACTCTTGTATTTGTTCTC	945
DB	601	ACTACCTAAACAGCAAGCTGCTTTTCACTCTTCTTGGAACTCTTGTATTTGTTCTC	660
QY	946	CTAAGTACCTCTGCTGCTGCAACCGGTCTGATAGTGGCTATGTTATCAAGAGCTA	1005
DB	661	CTAAGTACCTCTGCTGCTGCAACCGGTCTGATAGTGGCTATGTTATCAAGAGCTA	720
QY	1006	TACTTTGGAAGGCACTCAACTGACCGAGAGTTGCGCTTATCATGCTTATGCGCTATCTT	1065
DB	721	TACTTTGGAAGGCACTCAACTGACCGAGAGTTGCGCTTATCATGCTTATGCGCTATCTT	780
QY	1066	TCTTATATGCTTGTGAGCTTTTCGACTGAGCGGTATCTCATCTGTTTCTGTGGT	1125
DB	781	TCTTATATGCTTGTGAGCTTTTCGACTGAGCGGTATCTCATCTGTTTCTGTGGT	840
QY	1126	ATTGTGATGCTCCATTAACATGCGACATGTAAACGAGAGCTCAAGATTAACACAAAG	1185
DB	841	ATTGTGATGCTCCATTAACATGCGACATGTAAACGAGAGCTCAAGATTAACACAAAG	900

QY	1186	CATACCTTTGCAACTTTCTGATTTCTTCGCGAGACATTTATTTCTTGTATGTTGGAATG	1245
DB	901	CATACCTTTGCAACTTTCTGATTTCTTCGCGAGACATTTATTTCTTGTATGTTGGAATG	960
QY	1246	GATGCTTTGGACATTTGACAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA	1305
DB	961	GATGCTTTGGACATTTGACAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA	1020
QY	1306	GTGAGCTCAATCTCAATGGGCTCTGCTCATGTTTGAAGAGCAGCGCTTCTGTTCCGTTA	1365
DB	1021	GTGAGCTCAATCTCAATGGGCTCTGCTCATGTTTGAAGAGCAGCGCTTCTGTTCCGTTA	1080
QY	1366	TCGTTTCTATCTAATCTAGCCAAAGAAATCAAGCGAGAAATCAACTTTAAATGACAG	1425
DB	1081	TCGTTTCTATCTAATCTAGCCAAAGAAATCAAGCGAGAAATCAACTTTAAATGACAG	1140
QY	1426	GTTCGATTTTGGTGGTCTGCTCATGAGAGGTGCTGATCTTATGGCTTTTGCATACAC	1485
DB	1141	GTTCGATTTTGGTGGTCTGCTCATGAGAGGTGCTGATCTTATGGCTTTTGCATACAC	1200
QY	1486	AAGTTTACAGGGCGGCGCACACAGATGTAACGCGGAATGCAATCATGATCACGATGAG	1545
DB	1201	AAGTTTACAGGGCGGCGCACACAGATGTAACGCGGAATGCAATCATGATCACGATGAG	1260
QY	1546	ATAACTGCTCTCTTTTATAGCACAGTGGTGTGTTGATGTCGACCAACCACTCATAGC	1605
DB	1261	ATAACTGCTCTCTTTTATAGCACAGTGGTGTGTTGATGTCGACCAACCACTCATAGC	1320
QY	1606	TACCTATTACCGCACCAGAACGCCACACGAGCATGTTATCTGATGACAAACCCCAAAA	1665
DB	1321	TACCTATTACCGCACCAGAACGCCACACGAGCATGTTATCTGATGACAAACCCCAAAA	1380
QY	1666	TCCATACATATCCCTTTTGTGACCAAGACTCGTTTCATTGAGCCCTTCAAGGAACCAAT	1725
DB	1381	TCCATACATATCCCTTTTGTGACCAAGACTCGTTTCATTGAGCCCTTCAAGGAACCAAT	1440
QY	1726	GTGCTCGGCTGACAGTATACGTGGCTTTTGACACGGCCCACTCGAACCGTGATTTAC	1785
DB	1441	GTGCTCGGCTGACAGTATACGTGGCTTTTGACACGGCCCACTCGAACCGTGATTTAC	1500
QY	1786	TACTGGAGACAAATTTGATGACTCTTTCATGCGACCGCTTTTGGAGGTCTGGCTTTGTA	1845
DB	1501	TACTGGAGACAAATTTGATGACTCTTTCATGCGACCGCTTTTGGAGGTCTGGCTTTGTA	1560
QY	1846	CCCTTTGTTCCAGGTTCTCCAACTGAGAGAAACCTCTCTGATCTTTAGTAAGGCT	1899
DB	1561	CCCTTTGTTCCAGGTTCTCCAACTGAGAGAAACCTCTCTGATCTTTAGTAAGGCT	1614

RESULT 5

RESOLUTION	AY685183	1617 bp	mRNA	linear	PLN 16-AUG-2004			
LOCUS	Arabidopsis thaliana sodium proton exchanger (NHX1) mRNA, complete cds.							
DEFINITION	Arabidopsis thaliana sodium proton exchanger (NHX1) mRNA, complete cds.							
ACCESSION	AY685183							
VERSION	AY685183.1	GI:51094439						
KEYWORDS	Arabidopsis thaliana (thale cress)							
SOURCE	Arabidopsis thaliana							
ORGANISM	Arabidopsis thaliana							
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.							
REFERENCE	1. (bases 1 to 1617)							
AUTHORS	Wang, D., Zhang, J.L. and Zhang, J.W.							
TITLE	Direct Submission							
JOURNAL	Submitted (14-JUL-2004) Agronomy College, Institute of Agrobiotechnology, Lanzhou, Gansu 730070, China							
FEATURES	Location/Qualifiers							
source	1..1617	/organism="Arabidopsis thaliana"						
		/mol_type="mRNA"						
		/db_xref="taxon:3702"						
gene	1..1617							


```

RESULT 7
AY189676
LOCUS      AY189676               1723 bp      mRNA      linear      PLN 20-NOV-2003
DEFINITION Brassica napus Na+/H+ vacuolar antiporter mRNA, complete cds.
ACCESSION  AY189676
VERSION     AY189676.1  GI:37778921
KEYWORDS
SOURCE      Brassica napus (rape)
ORGANISM    Brassica napus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 1723)
            Wang, J., Zuo, K.-J., Wu, W.-S., Song, J., Sun, X.-F., Lin, J., Li, X.-F.
            and Tang, K.-X.
            Molecular cloning and characterization of a new Na+/H+ antiporter
            gene from Brassica napus
            DNA Seq. 14 (5): 351-358 (2003)
REFERENCE   2  (bases 1 to 1723)
            Wang, J., Zuo, K.-J., Wu, W.-S., Sun, X.-F., Li, X.-F. and Tang, K.-X.
            Direct Submission
            Submitted (30-NOV-2002) Institute of Genetics, Life Sciences, Fudan
            University, Handan 220, Shanghai 200433, China
FEATURES             Location/Qualifiers
     1..1723
         /organism="Brassica napus"
         /mol_type="mRNA"
         /db_xref="taxon:3708"
         169..1716
         /note="BrNhx1; similar to other Na+/H+ antiporter genes;
         sodium/hydrogen exchanger superfamily"
         /product="Na+/H+ vacuolar antiporter"
         /protein_id="AAO38856.1"
         /db_xref="GI:37778922"
         /translation="MDSLVSKPLSLSTSDHASVVALNLFVALLCACIVLGHLEENR
WNSITALLGLGTSVILIGSKSHLLVFSDEDFFIYLLPFIIFNAGFQVKKQ
FFRNFVTIMLGAIGTVVSCVTITLGVTFPKLIDIGFDLGDYLAIGAIPTADSVQ
TLVNLNODETELLYSLVFGVEGVNDATSVVFNAIQSPDLFHLNHEAAFOLLGNFMYL
FLSLTLGAVATGLISAVYIKKLYFGRHSDREEVALLMMLMAYLSYMLAEIPLFSLGILT
VFFGCIVMNHYTHNVTSSGVTTKHTFATLSFLAEAFIPLYVGMIDLDTKRWFSVD
SPGTSVAVSLIMGLMWLGRAAFVFPFLSFLSNLSKQSEKIDIKQOVWVWAGLMBG
AVSMALAYNKTRSGHTELRGNAMITSITIVCLFSTNVFGLMKPLIRHLMFPQSTT
TSMLSDDNTPKSLHMLPDLDDGEQDQSFVEFGSHHDVPRPDSLRGLRMPARTVHHYWR
QFDDSNH"
ORIGIN
Query Match      54.2%; Score 1180; DB 8; Length 1723;
Best Local Similarity 86.7%; Pred. No. 4.4e-253;
Matches 1339; Conservative 0; Mismatches 190; Indels 15; Gaps 3;

Qy  280  ATAACAATGTGGATCTCTAGTCGAAACTGCCCTTCGTTATCGACATCTGATCAGCGCT 339
Db  163  AAATCAATGTGGATCTCTAGTCGAAACTGCCCTTCGTTATCGACATCTGATCAGCGCT 222
Qy  340  TCTGTGGTTCGGTGAATCTCTTTGTTCACATCTTTGTGCTGTGATGTTGTTCTTGGTCAT 399
Db  223  TCTGTGGTTCGGTGAATCTCTTTGTTCACATCTTTGTGCTGTGATGTTGTTCTTGGTCAT 282
Qy  400  CTTTGTGGAGAGATAGATGATGAACCAATCCATCAGCGCTTGTGATTTGGGCTAGGC 459
Db  283  CTTTGTGGAGAGATAGATGATGAACCAATCCATCAGCGCTTGTGATTTGGGCTAGGC 342
Qy  460  ACTGTGTTTACCATTTCTTGATAGTAAAGGAAAAAGCTCGCATCTTCTCGTCTTTAGT 519
Db  343  ACTAGTGTACCATTTCTTGATAGTAAAGGAAAAAGCTCGCATCTTCTCGTCTTTAGT 402
Qy  520  GAAGATCTTTCTTCATATATCTTTTGGCCACCATTATATTCATGAGGGTTTCAAGTA 579
Db  403  GAAGATCTTTCTTCATATATCTTTTGGCCACCATTATATTCATGAGGGTTTCAAGTA 462

```

```

Qy  580  AAAAAGAAGCAGTTTTTTCCGCAATTTCTGTCGACTATTATGCTTTTGGTGTCTGTTGGGACT 639
Db  463  AAAAAGAAGCAGTTTTTTCCGCAACTTCGTGACGATTTATGCTCTTTTGGTGTCTATTGGAACT 522
Qy  640  ATTATTTCTTGGCAAAATCATATCTCTAGGTGTAAACACAGTTCTTTTAAAGAAGTTGGACATT 699
Db  523  GTTGTCTCTTGGCACTGTCAATACTCTAGGTGTAAACAGTTCTTTTCAAGAAATCGACATT 582
Qy  700  GGAACCTTTGACCTTGGGTGATTAATCTTGCTATTGGTGCCATATTTGCTGCAACAGATTCA 759
Db  583  GGGACCTTTGACCTTGGGTGATTAATCTTGCAATTTGGTGCCTATATTGGGGCAACAGATTCT 642
Qy  760  GTATGACACTGCAAGTTCTGAAATCAAGACGACACCTTTGCTTTACAGCTCTGTATTTC 819
Db  643  GTGTGCACTGCAAGGTGCTGAATCAAGATGAGACACCTTTGCTTTACAGCTCTGTATTTC 702
Qy  820  GGAGAGGGTGTGTGAAATGATCAACGCTCAGTTGTGTGCTTCTTCAACGGGATTCAGAGCTTT 879
Db  703  GGAGAAGGTGTGTGAAATGATGCCACATCAGTTGTGTGCTTCTTCAACGGCATTCAGAGCTTT 762
Qy  880  GATCTCATCTACCTAAACACGAAAGCTGCTTTTCACTCTTCTTGGAAAATCTTCTGTATTG 939
Db  763  GACCTCACACACCTTAAACCATGAAGCTGCTTTTCACTCTTCTTGGAAAATCTTCACTGTATTG 822
Qy  940  TTTCTCTTAAGTACTTGTGCTGTCGCAACCGGTCTGATAAGTGCGTATGTTATCAAG 999
Db  823  TTTCTCTTACGACATTTGCTGTGCTGCACTGGTCTGTGATAAGTGCGTATGTCATCAA 882
Qy  1000  AAGCTATACTTTTGAAGGCACTCAACTGACCG---AGAGGTTGCGCTTATGATGCTTATG 1056
Db  883  AAGCTATACTTTTGAAGACACTCAACCGACGAGAGAGGTTGCGCTTATGATGCTTATG 942
Qy  1057  GCGTATCTTTCTTATATGCTTGTGAGCTTTTGCATTTGAGCGGTATCTCTACCTGTGTTT 1116
Db  943  GCATATCTTTCTCATACATGCTTGTGAGCTATTTGCCCTTGAGTGTGTTATTTCTCACTGTGTTT 1002
Qy  1117  TTCTGTGCTATGTGATGTCCTCATTTACATACGTCGACAAATGTAAACGAGAGCTCAAGAATA 1176
Db  1003  TTCTGTGCTATGTGATGTCCTCATTTACGTTGGCACAAACGTAAACGAGAGCTCAGGAGTA 1062
Qy  1177  ACAACAAAGCATACCTTTTGCAACTTTGTCTCATTTCTTCCGGAGACATTTATTTTCTGTAT 1236
Db  1063  ACTACCAAGCATACCTTTTGTCTACTTTCTGCTTCTTCCGGAGAGCTTTTATTTTCTTCTTAC 1122
Qy  1237  GTTGGATGATGCTCTGGACATTTGACAAAGTGGAGATCCGTGAGTGACACACCCGGGACA 1296
Db  1123  GTCGGGATGATGATGATGGAATCGACATCGAGAAGTGGAGATTCGTGAGTGCAGCCCGGGACA 1182
Qy  1297  TCGATCGCAGTGAAGCTCAATCCTTAATGGGTCGTGCTCATGTTTGAAGAGCAGCGCTTCGTC 1356
Db  1183  TCGGTTGAGTGAAGCTCAATTCGATGGGTCGTGCTCATGCTTTGGAAGAGCAGCTTTTGTG 1242
Qy  1357  TTTCCGTTATCGTTTCTATCTAATAGCCAAAGAAATCAAAAGCGAGAAATAACAACCTTT 1416
Db  1243  TTTCTCTCTTCTTCTTATCAAACTCTGTCCAAGAAAAAATCAGAGCGAGAGATCGATATC 1302
Qy  1417  AACATGACAGTTGTGATTTGGTGTCTGGTCTCATGAGAGGTGCTGTATCTATGGCTCTT 1476
Db  1303  AAGCAGCAAGTTGTGATCTGGTGGGCTGGTCTGATGAGAGGTGCTGTCTCTATGGCTCTT 1362
Qy  1477  GCATACAAACAAAGTTTACAAGGGCGGGCACACAGATGTACCGGGAATGCAATCATGATC 1536
Db  1363  GCCTAACAAATGATTTACAGATCAGGACACACTGAATTTGGCGGGAATGCATCATGATT 1422
Qy  1537  ACGAGTACGATAACTGTCTGTCTTTTATGACACAGTGGTGTGTTTGGTATGCTGACCAACCA 1596
Db  1423  ACCAGTACTATAACCGTTTGTCTTTTATGACCAACATGCTGTGTTGGTATGTTGACAAAACCG 1482
Qy  1597  CTGATAGCTACCTATTATACCGCACACAGAAACGACACGACGAGCATGTTTATCTGATGACAC 1656
Db  1483  CTCATTAGACACTGATGCCCCCATCAAAAGTACAACCCACGACATGTTTATCCGACGACAAAC 1542
Qy  1657  ACCCCAAAATCCATACATATCCCTTTGTT-----GGACCAAGACTCGTTCATTGAG 1707

```

```
Db 1543 ACTCCGAAGTCTCTCACATGCGCTCTCGATGGCGAGCAGCAAGATTCATTGCTTGAG 1602
QY 1708 CCTTACAGGGAACACCAAT--GTGCTCGGCTCGAGATATAGTGGCTTCTTGACACGG 1764
Db 1603 TTCTCTGGGAGCACCACATGACGTGCGCGACCGACAGCCTTCGGGGTTTCTGTAGCGT 1662
QY 1765 CCACACTCGAACCGTGCATTACTACTGAGACAAATTTGATGACTC 1808
Db 1663 CCAGCAGCAGCTGTGCATCACTACTGAGACAAATTTGATGACTC 1706

RESULT 8
AF490586 1641 bp mRNA linear PLN 04-APR-2002
LOCUS Arabidopsis thaliana Na+/H+ exchanger 2 (NHX2) mRNA, complete cds.
DEFINITION AF490586
ACCESSION AF490586
VERSION AF490586.1 GI:19919839
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 1641)
AUTHORS Yokoi,S., Quintero,F.J., Cubero,B., Ruiz,T., Bressan,R.A.,
Hasegawa,P.M. and Pardo,J.M.
TITLE Differential expression and function of Arabidopsis thaliana NHX
Na+/H+ antiporters in the salt stress response
JOURNAL Plant J. (2002) In press
REFERENCE 2 (bases 1 to 1641)
AUTHORS Quintero,F.J., Cubero,B. and Pardo,J.M.
TITLE Direct Submission
JOURNAL Submitted (07-MAR-2002) Biologia Vegetal, IRNASA-CSIC, Avda. Reina
Mercedes, 10, Sevilla, Sevilla 41012, Spain
FEATURES
source
1..1641
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/chromosome="3"
/ecotype="landsberg erecta"
gene
1..1641
/gene="NHX2"
1..1641
/gene="NHX2"
/codon_start=1
/product="Na+/H+ exchanger 2"
/protein_id="AA08403.1"
/db_xref="GI:19919840"
/translation="MTMFASLTSKMLSVSTSDHASVSLNLFVALLCACIVIGHLLER
NRWNESITALLIGTGVVILLISRGKNSHLLVPSDELFTYLLPPIIPNAGQVKK
KQFRNFVTHAFGAITGVVSCGTIISIGAIQFFKLDIGTDFDGLAIGAFRAIDS
TQLVLNODETPLLYSLVGGVNDATSVLFNAIOSFDLTHLNHNAEFOFLGNPF
YLFSLTGAVTHYTHNVTRESSRITTKHAFATLSPLAETFIPLYGMDALDIKWRPVS
TVFFCGIYVMSHYTHNVTRESSRITTKHAFATLSPLAETFIPLYGMDALDIKWRPVS
DSPGTSVAVSSILMGLVLMGRAAFVPLSLFSLNLAKHQSEKISIKOOVVIWAGLME
GAVSLAYNKFTRSGHTLRGNALNMITSTIVCLFSTWVFGMLTKPLIRYIMPHOKA
TSTYSMLSDSDTPKSIHPLLDGEQLDSFELPGSHQDVPRPNSLRGLMRPRTVHY
YWRQDDAFMRPVFGGGRFVFPVPGSPTERSNDLSKP"

Query Match 52.4%; Score 1141.8; DB 8; Length 1641;
Best Local Similarity 82.0%; Pred. No. 1.5e-244;
Matches 1346; Conservative 0; Mismatches 277; Indels 18; Gaps 2;

QY 280 ATAAACAATGTTGGATTCTCTAGTTCGAAACTGCCCTTCGTTATCGACATCTGATCAGCT 339
Db 1 ATGACAATGTTCCGCTCTTTAACTCTTAAATGCTATCGGTGCTCAACTCTGATCAGCA 60

QY 340 TCTGTGGTTCGTTGAATCTCTTTGTTGCACTCTTTGCTGCTGCTGCTGCTGCTGCTGCT 399
Db 61 TCTGTGCTTCACTTAAATCTCTTTGCTGCTTCTATGCTGCTGCTGCTGCTGCTGCTGCT 120
```

```
QY 400 CTTTGGAGAGAAATAGATGAATCAATCCATCAGCGCTTGTTGATTGGGCTAGGC 459
Db 121 CTTTGGAGAGAAATCGATGGATGAACGAATCCATCAGCTGCTTATGATTGGGCTGGC 180
QY 460 ACTGTTGTACCAATTTTGTGTTAGTAAAGAAAAAGCTCGCATCTTCTGCTCTTTAGT 519
Db 181 ACTGTTGTGCTCATATGTTGATTAGTAGAGGAAAAAACTCACATCTGTTGGTCTTTAGT 240
QY 520 GAAGATCTTTTCTTCATATCTTTTGGCCACCCATATATTAATCAATGCAGGGTTTCAAGTA 579
Db 241 GAAGATCTTCTTCTTATATATCTTTTGGCCACCCATAATATCAATGCAGGGTTTCAAGTA 300
QY 580 AAAAAGAAAGCAGTTTTTCCGCAATTTCTGACTATTTATGCTTTTGGTGTCTGTGGGACT 639
Db 301 AAAAAGAAAGCAGTTTTTCCGAAATTTTGTAACTATTAATGGCTTTTGGCCCAATGGGACC 360
QY 640 ATTATTTCTTGCAATCATATCTCTAGGTGTAACACAGTCTTCTTAAGAAGTTGGACATT 699
Db 361 GTAGTTTCTTGCAACCAATAATCTCTAGGTGCAATTCAGTTCTTTAAGAAATTTAGACATT 420
QY 700 GGAACCTTTGACTTTGGGTGATTCTTCTGATTGTTGTCATATTTGCTGCAACAGATTCA 759
Db 421 GGGACCTTTGACTTTGGGCGATTTTCTGCAATCGCGCCATATTTGCTGCAACCGACTCT 480
QY 760 GTATGTACACTGCAGGTTCTGAATCAAGACGAGACACCTTTTGTCTTTACAGTCTTCTATTTC 819
Db 481 GTATGTACACTGCAGGTTCTGAATCAAGACGAGACACCTTTTGTCTTTACAGTCTTCTATTTC 540
QY 820 GGAGAGGCTGTTGTAATGATGCAACGTCAGTGTGTCCTTCAACCGCATTCAGAGCTTT 879
Db 541 GGAGAGGCGTTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 880 GATCTCACTCACTTAACACGAGAGCTGCTTTTCACTCTTCTTGGAACTCTTGTGATTGTG 939
Db 601 GACCTCACCCACCTTAAACCATGAAGCAGCTTTTCAATTTCTTGGGAACCTTTTATATCTG 660
QY 940 TTTCTCTAAAGTACCTTCTGCTGCAACCGGTCTGATAAGTGCATGCTGTTATCAAG 999
Db 661 TTTCTCTGAGCAGCGGACTTGGTGTGCAACTGCTGCTGATGATGCTGATGCTGATGCTGATGCT 720
QY 1000 AAGCTATCTTTGGAAGGCACTCAACTGACCGAGAGTTCCTTATGATGCTTATGCGG 1059
Db 721 AAACCTGATTTTGGAAAGCACTCGACTGATCGAAGTGTGCTGCTGATGCTGCTGCTGCTGCT 780
QY 1060 TATCTTTCTTATATGCTTGTGCTGAGCTTTTCACTTGTGAGGCTATCCTCACTGCTGTTTTC 1119
Db 781 TATCTTTCTTATATGCTTGTGCTGAGCTATTCGCTTGTGCTGCTGCTGCTGCTGCTGCTGCT 840
QY 1120 TGTGTTATGTTGATGCTCCATTACACATGCGCAATGTAACGGAGAGCTCAAGAAATAACA 1179
Db 841 TGTGGGATGTTGATGCTCCATTACACTTGGCACTGATGCTGAGAGCTCAAGAAATTAAT 900
QY 1180 ACAAGCATACCTTTTGCAACTTTGTCTTCTTGGGAGACATTTATTTTCTTGTATGTT 1239
Db 901 ACCAAGCATGCTTTGCTTACTTTTGTGCTTCTGCTGAGACATTTTATTTTCTCTACGTT 960
QY 1240 GGAATGATGCTTGGACATTCGAATGAGAGATCCGTTGAGTGACACACCGGGAACATCG 1299
Db 961 GGAATGATGATGCTTGGACATTCGAATGAGAGATTCGTTGAGTGACACACCGGGAACATCA 1020
QY 1300 ATCCAGTGTAGCTCAATCTTAATGGTCTGCTGATGTTTGAAGAGCAGCGTTCTGCTTTT 1359
Db 1021 GTTGAGTGTAGCTCAATCTTAATGGTCTGCTGATGCTTGAAGAGCAGCTTTTGTCTTT 1080
QY 1360 CCGTTATCGTTTCTATCTAACTTAGCCAAAGAAATCAAAGCGAGAAATCAACTTTAAC 1419
Db 1081 CCTCTTTCTTTCTTATCAAACTTAGCCAAAGCAATCAGAGCGAGAAATCAGCATCAAG 1140
QY 1420 ATGCAAGTTGTGATTTGGTGTCTGCTCTCATGAGAGTGTCTGATCTATGGCTCTTGCA 1479
Db 1141 CAGCAAGTTGTGATCTGGTGGGCTGGTCTAATGAGAGTGTCTGATCTATGGCTCTTGCC 1200
```


Db 866 GGCCTGTGGTACACTAATATCTTGATCAATATCTCTTTAGGTGAATTAATTAACCTCTTCAA 925
Qy 687 GAAGTTGACATTTGGAACCTTTGACTTGGGTGATTAATCTTGGTATTTGGTGCCATATTTGC 746
Db 926 GGAATGGAACATTTGGCTCTCTAGACATTTGGAGATTTCTTAGCAATTTGGTCAATATTTGC 985
Qy 747 TSCAACAGATTTCAGTATGATACACTCGAGTTCTGAATCAAGACGACACACTTTGCTTTTA 806
Db 986 TCCGACAGATTCGTTTGCACACTCAGGTGCTTAATCAGATGAGACTCCATTAATCTTA 1045
Qy 807 CAGTCTTGTTATTCGAGAGGGTGTGTGAATGATCAACAGTCAAGTGTGGTCTTCAACGC 866
Db 1046 CAGTTTGGTTTTCGAGAGGGTGTGTGAATGATCAACAGTCAAGTGTGGTCTTCAATGC 1105
Qy 867 GATTGAGAGCTTTGATCTCACTCACTTAACCAAGAGTGTCTTTCAATCTTCTTTGGAAA 926
Db 1106 AATCAGAGTTTTCACCTCGTTAATACCACTCTAGAAATCTTCTCGAGTTTATTTGGCAG 1165
Qy 927 CTTCTGTGTTATTTCTCCTAAGTACCTTGTGGTGTCTCAACCGGTCTGATAAGTGC 986
Db 1166 CTTTGTGTTATTTATTTTAGCAAGCACTATGCTGGAGTGAATGTTGGTGGTTAGTGC 1225
Qy 987 GTATGTTATCAAGAGCTATACCTTTGGAAGCACTCAACTGACGAGAGGTTGCCCTTAT 1046
Db 1226 TTACATCATCAAAAAGTTGACTTTTGGAGGCACTCAACAGATCTGTAATTTGCTTTAT 1285
Qy 1047 GATGCTTATGGGTATCTTTCTTATATGCTTGTGAGCTTTTTCGACTTTGAGCGGTATCCT 1106
Db 1286 GATGCTTATGGCATACCTTTCTGATATCATGCTGAACCTGTTCTATTATGAGTGGCATCT 1345
Qy 1107 CACTGTGTTTCTGCTGATTTGATGCTCCATTTACATGATGGAACAATGTAACGGAG 1166
Db 1346 TACAGTATCTTTTGTGGATTTGATGTCAATATATACCTGGAACAATGTAACCTGAG 1405
Qy 1167 CTCAGAATAACAACAAGCATACCTTTGCAACTTTGTCAATTTCTGCGGAGACATTTAT 1226
Db 1406 TTCAAGAGTAACATCAAGAGTGCCTTTGCTACCTTTGTCATTTGTTGCTGAGACTTTCT 1465
Qy 1227 TTTCTTGTATGTTGAATGATGCTTGGACATGCAAGTGGAGATCCGTGAGTGACAC 1286
Db 1466 CTTTCTTATGTCGGGATGGATGCTTTTGGACATGGAAGTGGAGATTTGTCAGTGATAG 1525
Qy 1287 ACCGGGAACATGATCGCAGTGAGCTCAATCTATATGCTGCTGTCATGTTGGTGAAGAGC 1346
Db 1526 CCTCGGAACGTGATGCTGTTAGTGTGCTGCTGATGGGCTGTTGTTGTTGGGAAGAGC 1585
Qy 1347 AGCGTTCTGCTTTTCGGTTATCGTTTCTATCTAACTTAGCCAGGAAGATCAAGCGAGAA 1406
Db 1586 GGCCTTTGTGTTCCCTGTCAATTTTATCCAACCTTGGCAAGAAATCAACTAGTGAGAA 1645
Qy 1407 AATCAACTTTAATGACAGGTTGTGATTTGGTGGTCTGCTGCTCATGAGAGGTCGTATAC 1466
Db 1646 AATCAGCTTCAGGAACAAAATTATAATATGTTGGGCTGGGCTCATGAGAGCGCTGTATC 1705
Qy 1467 TATGCTCTTGATACACAAGTTTCAAGGCGGGGACACAGATGTCGCGGAAGTGC 1526
Db 1706 TATGGCACTTGATATAATCAGTTTCAAGGGGGGGCCATCTCAGTTGCGAGGAATGC 1765
Qy 1527 AATCATGATCAGGATAGCAATCTGCTGCTTTTATGACAGTGGTGTGTTGGTATGCT 1586
Db 1766 AATTATGATTACAAGCACCAATACCAATGTTCTATTACAGCACTGGTGTGTTGGTTAAT 1825
Qy 1587 GACCAACACACTATAAGTACTATTAACCGCACAGAACGCGCACACAGAGATGTTATC 1646
Db 1826 GACTAAACCTCTAATAAGGTTCTTGCTGCTCATCCCAAAACCAACAGCAGCATGCTCTC 1885
Qy 1647 TGATGACAACACCCCAATCATACATATCCCTTTTGTGGACCAAGACTCGTTCAATGA 1706
Db 1886 AGACCAATCCACTCCAAATCAATGGAGGACATTTCTCGAAGCGGCCAGGACTCTTT 1945
Qy 1707 GCCTTCAGGAACCAACATGTCCTCGGCTGACAGATATAGTGTGCTTTCTTGACACGCCC 1766
Db 1946 TGATGATAGTTTAAATTGGAGTTTATCGACCAACAGCAATTCGTGCATCTTCAACACTCC 2005

Qy 1767 CACTCGAACCGTGCATTACTACTGAGACAAATTTGATGACTCTCTTATGCGACCGCTTT 1826
Db 2006 AGCACACACTGTTTCATTACTATTGGCGAAAAGTTTGATAATGCGCTTCATGCGCCCTATGTT 2065
Qy 1827 TGGAGGTGCGTGGCTTTGTACCCCTTTGTTCCAGGTCTCTCCAACTGAGAGAAACCTCTCTGA 1886
Db 2066 TGGTGGCGGGTTTTGTGCGCTTCGTCTCTGGCTCCCAACAGAAAGGAGTGAACTTAA 2125
Qy 1887 TCTTAGTAAGCTTTGAGGGTAACTGTAAGAAAAGCTTTT 1925
Db 2126 TCTGCTCAATGGCAATGAGGTGTTGAACAAGATCTCT 2164

RESULT 11
AY513732
LOCUS
DEFINITION
Medicago sativa Na+/H+ antiporter mRNA linear PLN 07-AUG-2004
ACCESSION
AY513732
VERSION
AY513732.1 GI:46250920
KEYWORDS
SOURCE
ORGANISM
Medicago sativa
Medicago sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE
1 (bases 1 to 1752)
An,B.Y. and Zhang,X.S.
TITLE
Isolation and expression of MeNHX1 gene in alfalfa
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 1752)
An,B.Y. and Zhang,X.S.
AUTHORS
Direct Submission
TITLE
Submitted (27-DEC-2003) College of Life Sciences, Shandong
JOURNAL
Agricultural University, Daizong Street, Taian, Shandong 271018,
P.R. China
FEATURES
Location/Qualifiers
1..1752
/organism="Medicago sativa"
/mol_type="mRNA"
/cultiivar="WL323"
/db_xref="taxon:3879"
127..1752
/codon_start=1
/product="Na+/H+ antiporter"
/protein_id="AAS84487.1"
/db_xref="GI:46250921"
/translation="MAIEMTSIVSKLSMLSTSDHASVVSNNLFAVLLCACIVLGHLLLE
ENRMNRSIALLIGICTGVILLFSGGKSSHLVPSEDIFFYVLLPPIFNAGFQVK
KKQFFVNFMTITSGAIGTLISCVIITIGATFAPKMDIGLEIGDYLALGATFATD
SVCTQLVNDQETPLLSLVFGGVNDATSVLFNAIQSFDNLQNLPSALHFLGNF
LYLFASTLLGVVTGLLSAYVKKLYIGRHSITREVALMMLAYLSYMLALHTYLSGI
LTVPFCGIVMSHVTHNVTOSRITTKHSFATLSFVAEIFLYVGMADLDIEKWFV
SDSPGTSIAASSVLGLLIGRAAFVPLSFLSNLTKKSOHKISFRQOVIIMWAGLM
RGVMSALATNYQTMSTGHTQLRNAIMTITITVLFSTVFGLLTKPLRLLLPHPK
ITSSMTITSTPKSFIVPLLDGSEADLEGHEIHRPNSLRALLSTPTHTVHRLMR
KFDSDFRPVPFGGRGFPVFPFSGPSERNQNG"

CDS
39,48; Score 858; DB 8; Length 1752;
Best Local Similarity 72.08; Pred. No. 4.2e-181;
Matches 1148; Conservative 0; Mismatches 440; Indels 6; Gaps 2;

ORIGIN
Query Match 39,48; Score 858; DB 8; Length 1752;
Best Local Similarity 72.08; Pred. No. 4.2e-181;
Matches 1148; Conservative 0; Mismatches 440; Indels 6; Gaps 2;

Qy 290 TGGATTCTCTAGTGTGAAACTGCTTCGTTCATCGACATCTGATCAGCTTCTGTGGTTG 349
Db 140 TGACTTCTATGTTTCAAACTATCAATGTTATCCACTCCGATCATGCTTCTGTGTTT 199
Qy 350 CGTTGAATCTCTTTGTTGCACTTCTTTGCTGCTGATTTGTTCTTGGTCATCTTTTGGAG 409
Db 200 CTATGAACCTTGTGTTGGCACTTCTGTGCTGCTGATTTGTTGCTGCTTCTCGAGG 259
Qy 410 AGAATAGATGATGAACGAATCCATCATCCGCTTGTGTTGTTGGGCTAGGCACTGGTGTTA 469

```
Db 260 AGAATCGATGGATGAATCAATCACTACCTCTTTGATTTGATTTATTTGCACTGGTGTAG 319
Qy 470 CCAATTTTGTGTTAGTAAGGAAAGAGCTCGCATCTTCTCTGCTTTTAGTGAAGATCTTT 529
Db 320 TGAATTTTGTGTTAGTGGTGAAGAGTTCGCATATCTTGTGTTTCAAGTGAAGATCTTT 379
Qy 530 TCTTCATATATCTTTTGGCCACCATATATCAATGACAGGTTTCAAGTAAAAAAGAGC 589
Db 380 TCTTTATATACCTTCTGCGGCTATATATCAATGACAGGTTTCAAGTAAAAAAGAGC 439
Qy 590 AGTTTTTCCGCAATTTCTGACATATATGCTTTTGGTGTGCTGTTGGGACTATATTTCTT 649
Db 440 AGTTTTTGTCAACTTATGACTATACATCAATTTGGAGCTATTTGGCACAATTAATATCTT 499
Qy 650 GCACATATATCTCTAGTGTGTAACACAGTTCTTTAAAGAGTTGGACATATGGAACCTTTG 709
Db 500 GTGTCAATATACACGGGTGCTACTTTTGTCTTTTAAAGAGTATTTGGGCCACTGG 559
Qy 710 ACTTGGGTGATATCTTGTATTTGGTGCCATATTTGCTGCAACAGATTCAGTATGACAC 769
Db 560 AAATCGGCGATATCTAGCTATTTGGAGCAATATTTGCGCAACAGACTCTGTTGACAT 619
Qy 770 TGCAGTTCTGAATCAAGACGAGACCTTTCCTTTACAGTCTTGTATTCGAGAGGGTG 829
Db 620 TGCAGTGTCTAAATCAGGATGAGACACCTTTTATTTGTATAGTCTTGTATTTGGGGAAGTG 679
Qy 830 TTGTGAATGATCAACGCTGAGTTGTGCTTCAACGCGATTCAGAGCTTTGATCTCACTC 889
Db 680 TTGTGAATGATGCTACCTCAGTGGTCTTTTCAATGCAATCAAGCTTTGATCTTAACC 739
Qy 890 ACCTAAACCAAGAGCTGCTTTTCATCTTTGGAACCTCTTGTATTTGTTTCTCTAA 949
Db 740 AACTGAACCTTCAATGCAATGCAATCTTCTGGGCACTTCTGATTTGTTGTAGCA 799
Qy 950 GTACCTTGTGTTGGTGCAACCGGTCTGATTAAGTGGGTATGTTATCAAGAGCTATACT 1009
Db 800 GCACACTCTTGGGCTGTGACAGCTCTGCTCAGTCTTATGTTATTAAGAGCTGTACA 859
Qy 1010 TTGGAAGCACTCAACTGACGAGGTTGCCCTTATGATGCTTATGATGCTTATCTTCTT 1069
Db 860 TTGGCAGGCACTTCCAGATCTGAGGTTGCTCTTATGATGCTAATGCACTACCTCTCT 919
Qy 1070 ATATGCTTGTGAGCTTTTCCGACTTTGAGCGGTATCTCTACTGTTGTTTCTGTGTTATG 1129
Db 920 ATATGCTGCTGAGTTAACTATCTGAGTGGATCTTACCGTATCTTGTGTTATG 979
Qy 1130 TGAATGCCATPACATGGCAATGTAAACGAGAGCTCAAGATTAACAACAAGACATA 1189
Db 980 TTATGCTCATATATCTTGGCATAATGTGACGAGGTTCAAGATCACTACCAAGCAT 1039
Qy 1190 CTTTGGCACTTTGTCTATTTCTGGGAGACATTTATTTCTGTATGTTGGAATGGATG 1249
Db 1040 CTTTGTGCTACCTTGTCTTGTGAGATCTTTATCTCTCTTATGTTGTTGATGGATG 1099
Qy 1250 CTTTGGCACTTGAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGAGTGA 1309
Db 1100 CCTTGGACATTTGAAAATGGAATTTGTTAGTATAGTCTTGGACATCTATAGTGCAG 1159
Qy 1310 GCTCAATCCTAATGCGTCTGTTGATGTTGGAAGACGAGCGTCTCTTCCGTTATCGT 1369
Db 1160 GTTCAGTATTTGTTGGTCTAATCTTCTTGGGAGGAGCGGTTTCTTTTCTCTATCTCT 1219
Qy 1370 TTCTATCTAACTTAGCCAGAGATCAAGGAGAGAAATCACTTTAATCATGCGAGTTG 1429
Db 1220 TCTTATCAACTTGAATAAAAAATCAACAATCAGAGATTTCTCTCAGACAGCAAGTTA 1279
Qy 1430 TGAATTTGTTGCTGCTCTCATGAGAGGTTGTTATCTATGCTCTCTCATACACAGAT 1489
Db 1280 TCAITTTGTTGGGCTGGCTTATGAGAGGTTGCTGTTTCAATGGCACTTGGCTAATCATG 1339
Qy 1490 TTACAAGGCGCGGACACAGATGTACGCGGAATGCAATCATGATCACTGAGTACGATAA 1549
```

```
Db 1340 TCACATGTCGGGGCATACTCAACTACGTAGCAATGCAATCATGATAACGACCATCA 1399
Qy 1550 CTGCTGTCTTTTAGCACAGTGGTGTGTTGTTATGCTGACCAAAACCACTCATAACTACC 1609
Db 1400 CTGTTGCTCTTTTAGCACAGTGGTGTGTTGTTGCTGACTAGCCACTCATAGGCTTC 1459
Qy 1610 TATTACCCGACAGAAACGCCACCGACGACATGTTA---TCTGATGACAAACCCCAAAAT 1666
Db 1460 TACTACCTCATCTAAATCAACAGCAGATGACAAACACAGAAATCGACTACTCCAAAT 1519
Qy 1667 CCATACATATCCCTTTGTTGGACCAAGACTCGTTCAITTAGGCC---TTCAGGGAACCA 1723
Db 1520 CATTCATTTGCTCCACTTCTAGGAGATTCGCCAGATTTCTGAAGCTGATCTTGAAGCCATG 1579
Qy 1724 ATGTCCTCGCCTGACAGATATACGTGCTTCTTTCGACAGCGCCACTCGAACCGTGCAAT 1783
Db 1580 AAATTCACGACGACGACGCTTCTGCTTTTACTATCACTCAACTCAGCTGTTTCTATC 1639
Qy 1784 ACTACTGAGACAAATTTGATGACTCTTTCATCGGACCGCTCTTTGGAGGTCGTGCTTTG 1843
Db 1640 GATTATGCGGAAAGTTTTCATGATTCATTCATGCGTCTGTTTTCGTCGAGAGGTTTG 1699
Qy 1844 TACCTTTGTTCCAGGTTCTCAACTGAGAGAA 1877
Db 1700 TTCCTGTAGAACCTGGCTCACCAAGTGAACGAA 1733

RESULT 12
LOCUS AY456096 2232 bp mRNA linear PLN 23-NOV-2003
DEFINITION Medicago sativa Na+/H+ antiporter mRNA, complete cds.
ACCESSION AY456096
VERSION AY456096.1 GI:38373524
KEYWORDS Medicago sativa
SOURCE Medicago sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 2232)
AUTHORS Yang,Q.C., Wu,M.S. and Wang,P.Q.
TITLE The gene encoding Na+/H+ antiporter cloned from alfalfa
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2232)
AUTHORS Yang,Q.C., Wu,M.S. and Wang,P.Q.
TITLE Direct Submission
JOURNAL Submitted (01-NOV-2003) Turf & Forage Science, Chinese Academy of
Agricultural Science (CAAS), No.2 Yuanmingyuan West Road, Haidin,
Beijing 100094, China
FEATURES
source
1..2232
/organism="Medicago sativa"
/mol_type="mRNA"
/cultivar="Zhongmu No. 1"
/db_xref="taxon:3879"
336..1961
/notice="expression is salt-inducible"
codon_start=1
/product="Na+/H+ antiporter"
/protein_id="AAR19085.1"
/db_xref="GI:38373525"
/translacion="MAIEMSSIVSKLSMLSTSDHASVVMNLFVALLCACLVLGHLE
ENRMNNSITALLIGICTGVVILFSGKSHLIVFSDLFIFILLPPIIFNAGFQVK
KKQPFVNMFTISFGLISCVIITGATFAPKRMFDQPLEIGDYLAIGAIATD
SVCTQLVNDQDETPLYSLVFGVGVNDATSVFNATQSPDLNLPNSIALHFLNF
LTLFVAGTLLGVTLISAVYIKLYIGRHSITREVALMLMLVSLYSLATLVLGI
LTVFPCGIVNHSYTHNVNTOSSRTTKHSFATLSFAVEIFI FLVVGMDALDIKWKV
SDSPGTSIARSSVLLGILLIGRAAFVPLSFLSNLTQSKQHSQKHSFQOVLINWGLM
RGVSMALAYNQFTMSGRQLRSNAIMTSTITVLFSTVVGTLTLPILLLPLHPK
ITSSMTSTETPKSFIVPLQLRSDRSEADLEHGHEIHRPNSLRALLSTPTTTHVRLWR
KFDDSFMRPVFGGRGFVPEGPSERNQWG"
ORIGIN
```

Query Match		39.4%; Score 858; DB 8; Length 2232;	
Best Local Similarity		72.0%; Pred. No. 4.1e-181;	
Matches 1148; Conservative		0; Mismatches 440; Indels 6; Gaps 2;	
QY	290	TGGAATCTCTAGTGTGGAACCTGCCCTCGTATTCGACATCTGATCAGCTCTCTGTGGTTG	349
DB	349	TGTCTTCTATTGTTTCAAAACTATCAATGTTATCCACTTCGGATCATGCTTCTGTGTTT	408
QY	350	CGTTTGAATCTCTTTGTTGTCACCTCTTTTGCTGTGTTATGTTTCTTGGTCATCTTTTGGAG	409
DB	409	CTATGAACCTTGTTTTGGCACTTCTGTGTCTGTATTTGCTTGGTCATCTTCTCGAGG	468
QY	410	AGAATAGATGGATGAACGAATCCATCACCGCCCTTTGTTGATTTGGCTAGGCACCTGGTTA	469
DB	469	AGAATCGATGGATGAATGAATCCATCACTGCCCTTTTGAITGGTATTTGCACCTGCTAG	528
QY	470	CCATTTTGTGATTAGTAAAGAAAAGCTCGCATCTTCTCGTCTTTAGTGAAGATCTTT	529
DB	529	TGATTTTGTGTTTGTAGTGGTGGAAAAAGTTTCGCATATCTTGTGTTTTCAGTGAAGATCTTT	588
QY	530	TCCTTCATATATCTTTTGGCCACCATATATTTCAATGCAGGCTTTCAAGTAAAGAAAGC	589
DB	589	TCCTTATATACCTTCTCCGCCCTATATATTTCAATGCCGGGTTTCAAGTAAAGAAAGC	648
QY	590	AGTTTTTCCGAATTTTCGTGACTATTAATGCTTTTTTGGTGTCTTTGGGACATTAATTTCTT	649
DB	649	AGTTTTTGTCAACTTCATGACTATCACATCAATTTGGAGCTATTTGGCACATTAATACTT	708
QY	650	GCACAATCATATCTCTAGTGTGAACAGATCTTTTAAAGATTTGGACAATTTGGAACCTTTG	709
DB	709	GTGTCATATTAACCAACGGGTGCTACTTTTGTCTTTTAAAGAGATGGATTTTGGGCCACTGG	768
QY	710	ACTTTGGTGATTATCTTGCTATTGTTGGCTATTTTGTGCAACAGATTCAGTATGTACAC	769
DB	769	AAATTCGGCGATTATCTAGCTATTTGGAGCAATATTTGCCGCAACAGATCTGTGTTGCAAT	828
QY	770	TGCAGTCTCTGAAATCAAGACGAGACACCTTTGCTTTTACAGTCTTTGTTATTCGGAGAGGCTG	829
DB	829	TGCAGTGTCTAAATCAGATGAGACACCTTTATGTATAGTCTGTATTTTGGGAAGGTG	888
QY	830	TTGTGAATGATGCAACGTCTAGTTGTGTCTTCAACGCGAATTCAGAGCTTTGATCTCACTC	889
DB	889	TTGTGAATGATGCTACCTCAGTGGTCTTTTTCATATGCAATTCAAAGCTTTGATCTTAACC	948
QY	890	ACCTAAACACGAGCTGCTTTTTCATCTTCTTGGAAACTTCTTGTAATTTGTTTCTCTCTAA	949
DB	949	AACCTGAACCCCTCAATTTGCATTTGCATTTCTTGGGCACTTCTCGTATTTTGTGTAGCAA	1008
QY	950	GTACTTGTCTGTGTCGAACCGTCTGATAGTGCATGTTATCAAGAAGCTATACT	1009
DB	1009	GCACACTCCTTGGGTTGTACAGGTCGTCTCAGTGCCTATGTTATTTAAAGCTGTACA	1068
QY	1010	TTGGAAGGCACTCAACTGACCGAGAGTTGCCCTTATGATGCTTATGGCGTATCTTTCTT	1069
DB	1069	TTGGCAGGCACCTCACAGATCGTGAGGTTGCTCTTATGATGCTAAATGGCATACCTCTCCT	1128
QY	1070	ATATGCTTGTGAGCTTTTCGACTTGGCCGATTCCTCACCTGTGTTTTTCTGTGGTATTG	1129
DB	1129	ATATGTGGCTGAGTTAAACCTATCTGAGTGGCAATCTTACCGTATTCCTTTGTGGTATTG	1188
QY	1130	TGATGTCCCAATTACATATGCAAACTGAACGGAGAGCTCAAGAATAACAACAAGCATAT	1189
DB	1189	TTATGCTCATTTATCTTTGGCAATAATGTGACGCGAGTTCAAGNATCACCTACCAAGCATT	1248
QY	1190	CCTTTGCACCTTTGTCTATTTCTTGGGAGACATTTATTTTCTTGTATGTTTGGATGGATG	1249
DB	1249	CTTTTGTCTACCTTGTCTTTTGTGTCGAGATCTTTATCTTCTCTTATGTTTGGTATGATG	1308
QY	1250	CCTTGGACATTGACAGTGGAGATCCGTGAGTGAACACCGCGGAACATTCGATCCGAGTGA	1309
DB	1309	CCCTGGACATTGAAAATGGAAGTTTCTGTAGTATGTTCTCTGGAAACATCTATAGCTCGAA	1368

```

/gene="NHX"
/codon_start=1
/product="Na+/H+ antiporter"
/protein_id="AA072785.1"
/db_xref="GI:34484304"
/translation="MWSQLSLLSKMDALATSDHASVVSMMFVALLGCGIVIGHLL
ENRWNESITALLGLAGTVGVILLISGKSHLVFSEDLFFIYLLPPIIFNAGFOV
KKQFRFITILFEGAVTVLVSFTIISGALSIFKGLDLSGLADYLAICAFPAAT
DSVCTQLVNDODETLXSLVPEGVNDATSVLFNAIQSFDLTIIDHRLALOPMGN
FLYLFIASITILGATGLLSAYIIKKLYGRHSITREVALMLMAYLSYMLAEFLVLSG
LLTVLFCGVSHVSHYTHWNVRESSRVTHKAEATLSFVAEFLFLVGVHDALDIEKWRP
VSDSGTSVAVNSISLGLIMVGRAPVFLSLMNFASKSHSEKSLNQVIVWAGL
MRGASMALAYNQITFRSHQQLRGNAMITSTTVLVFSTVWFGLLAKPLIMFLPQP
KHFTSCSTVDLSPKAYLPLLEGHQYEDVGNHDDGTEPTIARPSRLMLNAPTH
TVHHYWRKFDSDSFMRPVFGRGFVFPVPGSPTEQSHNLADRT"

```

ORIGIN

Query Match 38.3%; Score 833.4; DB 8; Length 1656;
 Best Local Similarity 71.4%; Pred. No. 1.3e-175;
 Matches 1136; Conservative 0; Mismatches 431; Indels 24; Gaps 2;

```

QY 323 CGACATCTGATCAGCGCTTCTGGTGGTGAATCTCTTTGTCGACTTCTTGTGCTT 382
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
50 CCACTTCGATCATGCTTCTGGTCTCGATGATATGTTTGGCAGCTGCTCTGTGTT 109
QY 383 GTATTGTTCTTGGTCACTTTTGGAGAGATAGATGGATGAACGAATCCATCAGCGCT 442
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
110 GCATCGTAATTGTCATCTCTGGAGAGATCGCTGGATGAACGAGTCCATCTGCTC 169
QY 443 TGTGATTTGGGTAGCGACTGTGTACCATTTTGTGATTAAGTAAAGAAAGCTGCG 502
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
170 TACTTATAGGTTTGGCTAGTGGGTTGCAITCTGCTGATTAGTGGAGAAAGATTGCG 229
QY 503 ATCTTCTGCTTTAGTGAAGATCTTTCTTCATATATCTTTTGGCCACCATATATCA 562
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
230 ATCTTTTGGTTTTCAGTGAAGATCTTTCTTCATATACCTTCTCCCGATTATATTA 289
QY 563 ATGCAAGGTTTCAAGTAAAGAAAGACAGTTTTCGCAATTTCTGACTATTTATGCTTT 622
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
290 ATGCAAGGTTTTCAGTGAAGAGAGAGTCTTTCGCAATTTCTTCAATATATGTT 349
QY 623 TTGGTCTGTTGGGACTATTTCTTGGCAATCATATCTAGTGTGAACACAGTTCT 682
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
350 TTGGAGCTGTTGGTACATTTGGTATCAITTCACCATCATATCTTTTGGAGGTTGTCAA 409
QY 683 TTAAGAAGTGAACATGCACTTTGACTGGGTGATTTCTGCTATTTGGTGCATAT 742
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
410 TTAAGAAATTTGATATGTTCTCTGGACTTGGCAGACTATCTTCTATCGGTGCAATAT 469
QY 743 TTGCTGCAACAGATTCACTATGATACATGCACTGAGTTCTGAATCAAGACGAGACCTTTGC 802
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
470 TCGCTGCCACAGATTCTGTTGCAATTTGCACTGAGTGTCTCATCAGATGAGACCTTCTGC 529
QY 803 TTACAGTCTTGTATTCGAGAGGTTGTGTAATGATGCAACGTCAGTGTGGTCTTCA 862
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
530 TCTACAGTTTGGTGTGGTGGGCTGTTGTAATGATGCAACATCACTGAGTGTCTTTCA 589
QY 863 ACDCGATTTCAGAGCTTGCATCTCACTCACTTAAACACGAGAGCTGTTTCTCTCTTG 922
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
590 ATGCGAATTCAGAGCTTGCATCTCAACAAATCGATCAAGAAATTCCTTACAAATTTATGG 649
QY 923 GAAACTTCTTGTATTGTTTCTTCTTAAGTACCTTCTGTTGGTCTGCAACCGGTCTGATA 982
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
650 GCAACTTCTTATATTATTATTCGCAAGCACTATTTCTTGGAGCATTTACTGGCTGCTCA 709
QY 983 GTGCGTATGTTATCAAGAGCTATATCTTTGGAAGGCACTCAACTGACCGAGAGTTGCC 1042
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
710 GTGCTTACATATCAAAAGTTGTAATTTGGAAGGCACTCCACTGATCGGAGGTTGCTT 769
QY 1043 TTATGATGCTTATGCGGTATCTTTCTTATATGCTTGTGAGCTTTTTCAGTTGAGCGTA 1102
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
770 TAATGATGCTTATGCTTATCTTATCTTATGCTGTTGCTGAACCTTTTCTATTAAAGCGAA 829

```

```

QY 1103 TCCTCACTGTGTTTTTCTGTGATTTGTGATGTCCATTACATGGCACAAATGTAAACGG 1162
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
830 TTCTTACAGTGTCTTCTGTGGAATTTGTCAATGTCCTCAATTAAGCTGGCACAACTGACAG 889
QY 1163 AGAGCTCAAGAAATAACAACAAGCATACCTTTTGCNACTTTGTCACTTTCTTGGGAGACAT 1222
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
890 AGAGCTCAAGAGTAACCAACCAAGCATGCTTTTGAACACTGTCTTTTGTGCTGAGGTTT 949
QY 1223 TTATTTTCTGTATGTTTGAATGATGCTTGGACATTTGACATTTGCAAGTGGAGATCCGTGAGTG 1282
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
950 TCCTCTTTCTATATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1009
QY 1283 ACACACCGGGAACATCGATCGAGTGAATCAATCTAATGGGTCTGCTGATGTTGGAA 1342
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1010 ATAGTCTCTGGCACTTCTGTTCTGTGAGTTCCATATTTGCTTGTCTGATCATGTTGGAC 1069
QY 1343 GAGCAGGCTTCTGTTTCCGTTTATCTTCTATCTTAACCTAGCCNAGAAATCAAAGCG 1402
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1070 GAGCAGCTTTTGTCTTCCCTTATCATGGTTTAATGAACCTTTGCCAAGAAATCACATAGTG 1129
QY 1403 AGAAATCAACTTTAAACATGCAAGTTGATTTGGTGTCTGTTCTCATGAGAGTGTG 1462
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1130 AAGAGTCTCCTCAACAGCAGGTGTCATATGTTGGCTGGTCTTATGAGAGTGTG 1189
QY 1463 TATCTATGGCTTCTGCATACAACAAAGTTTACAAGCGCGGCGCACACAGATGTACGCGGA 1522
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1190 TTTCCATGGCACTTGTCTTATTAATCAGTTTACGAGTCAAGGCGCACACAGCTGAGGGGA 1249
QY 1523 ATGCAATCATGATCAGAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATG 1582
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1250 ATGCAATCATGATCACAAGCACTACACTGTTGCTCTTATTCAGTACATGTTGTTGGGT 1309
QY 1583 TGCTGACCAACCACTCATTAAGTCTATTTACCGCACCAAGCAAGCCACCAACGAG- 1637
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1310 TGCTGGCAAGGCTCTCATATGTTTTTGTGCTCTCAACCAAAACACTTTACTAGTTGCA 1369
QY 1638 ----CATGTTATCTGATGACAAACCCCAAAATCCATACATATCCCTTTTGGACCAAG 1693
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1370 GCACCGTGTGAGTCTGGAAAGTCCAAAGCATACTTGCCTCTCTTGGGGCCATCAAG 1429
QY 1694 ACTGTTTCATTTGAGCTTTCAGGGAACCAATG- 1738
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1430 ATTATGAAGTTGATGTGGGGAACCATGACGATGCACTGAGCCAACTATAGCTCGACCTA 1489
QY 1739 ACAGTATACGTTGCTTGTGACACGGCCACTCGAAACGTCATTTACTTCTGAGACAAAT 1798
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1490 GTAGCTTCGATGCTTCTAAATGACCTCTCACACAGTCCATCATATTGGGCGCAAT 1549
QY 1799 TTGATGACTCTTTCATGCGACCCCTTCTTTGAGGTCGTGGCTTTGTACCCCTTTGTCCAG 1858
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1550 TTGATGACTCTTTCATGCGGCTGTGTTGTTGGCGGGGTTTGTACCTTTTGTCCCTG 1609
QY 1859 GTTCTCCAATCGAGAGAAACCTCTCTGATCT 1889
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1610 GTTCACCTACTGAAACAAAGCACCCATAATTT 1640

```

RESULT 14

E63046 Na+/H+ antiporter protein and gene encoding it.
 LOCUS E63046 1668 bp DNA linear PAT 31-JAN-2002
 DEFINITION Na+/H+ antiporter protein and gene encoding it.
 ACCESSION E63046
 VERSION E63046.1 GI:18628471
 KEYWORDS JP 2000157287-A/1.
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 1668)
 AUTHORS Shono, M., Hayakawa, T. and Tanaka, A.
 TITLE Na+/H+ antiporter protein and gene encoding it
 JOURNAL Patent: JP 2000157287-A 1 13-JUN-2000;
 COMMENT PLANTECH RESEARCH INSTITUTE
 OS Atlixplex gmelini

[illegible]

Search completed: August 28, 2005, 05:36:17
Job time : 9539 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 28, 2005, 02:09:40 ; Search time 7195 Seconds
(without alignments)
11522.443 Million cell updates/sec

Title: US-10-617-624-1
Perfect score: 2178
Sequence: 1 cctctctgttccttcctcg.....aaaaaaaaaaaaaaaaaaaaa 2178

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	671.6	30.8	2080	3	AY105332 Zea mays
2	630.6	29.0	3272	3	AY109416 Zea mays
3	595.6	27.3	651	6	C99909 C99909 Arab
4	487.2	22.4	834	6	CA767092 AF53-Rpt
5	478.8	22.0	1449	9	CL973674 OsIFCC024
6	435.8	20.0	483	5	BP570332 BP570332
7	432.8	19.9	966	7	CK360919 EST706997
8	432	19.8	433	1	AV792419 AV792419
9	429.4	19.7	629	1	AV825792 AV825792
10	422.4	19.4	448	6	CD531888 12G22 Ara
11	416.6	19.1	733	5	BU004460 QGSE06.Y
12	416.2	19.1	827	7	CO094724 GR_Eal7A
13	415.8	19.1	1212	2	BE420587 HWM000.D1
14	415	19.1	827	7	CO085721 GR_Ea03A
15	414.2	19.0	852	6	CB681657 OSJNEf08D
16	412.4	18.9	767	7	CF479378 RTW3.23
17	411	18.9	743	6	CA484823 WHE4311.B
18	409.6	18.8	690	5	BQ865196 QGC2a03.Y
19	408	18.7	420	1	AV788758 AV788758
20	406.2	18.7	719	4	BJ312595 BJ312595
21	401.4	18.4	804	7	CO100982 GR_Eb002
22	400.8	18.4	615	5	BQ589958 S015138-0
23	397.8	18.3	404	5	BP609318 BP609318
24	396.4	18.2	665	4	BI933988 EST553877

25	396.2	18.2	786	7	CF208932	CF208932	CAB20004
26	396	18.2	719	5	BU039126	BU039126	PP_LRa000
27	385	17.7	658	7	CO099045	CO099045	GR_Ea23L
28	381.2	17.5	420	5	BP565077	BP565077	BP565077
29	380.4	17.5	772	6	CD486155	CD486155	CFUS6.4D1
30	375.4	17.2	830	7	CK862028	CK862028	33159 In
31	375.2	17.2	619	5	BU926933	BU926933	sa893e08.
32	373	17.1	589	7	CN909560	CN909560	030123ABL
33	370	17.0	819	6	CB671396	CB671396	OSJNE04P
34	370	17.0	833	6	CB668797	CB668797	OSJNE016N
35	365.8	16.8	369	1	AV815619	AV815619	AV815619
36	359.6	16.5	736	6	CA238161	CA238161	SCEQPLS05
37	351.4	16.1	761	6	CA197063	CA197063	SCBFAD109
38	350.8	16.1	756	6	CA243274	CA243274	SCBGLF109
39	350.6	16.1	607	5	BO612167	BO612167	sap80d01.
40	349.8	16.1	802	5	BO512490	BO512490	EST619905
41	346.8	15.9	709	7	CO528231	CO528231	3530_1.18
42	345.6	15.9	664	6	CA246092	CA246092	SCEZFL508
43	345	15.8	666	6	CA216351	CA216351	SCRLFL402
44	343.8	15.8	542	7	CN890706	CN890706	010513AAx
45	343.4	15.8	706	4	BJ291707	BJ291707	BJ291707

ALIGNMENTS

RESULT 1
AY105332
LOCUS AY105332 2080 bp mRNA linear HTC 16-OCT-2002
DEFINITION Zea mays PC0131050 mRNA sequence.
ACCESSION AY105332
VERSION AY105332.1 GI:21208410
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1 (bases 1 to 2080)
AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitesitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
TITLE Zea Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 2080)
AUTHORS Coe,E.H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, the
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
maize cDNA sequences is either Virginia Walbot, Stanford or Pat
Schnable, Iowa State, then clones may be requested from ZmDB:
www.zmdb.iastate.edu.

FEATURES
Location/Qualifiers
1..2080
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="MaizeDB:637649"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Consensus
Library"
/note="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed DuPont contigs; this resource was
assembled by DuPont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"

ORIGIN
Query Match 30.8%; Score 671.6; DB 3; Length 2080;

Best Local Similarity 65.5%; Pred. No. 7.4e-149; Matches 1029; Conservative 0; Mismatches 534; Indels 7; Gaps 3;									
QY	318	GTATATCGACATCTGATCAAGCTTCTGTGGTGGCTTGAATCTCTTTGTGGCACTTCTTTG	377						
Db	225	GCTCTCGGCTCGGATCAGACGCCATCGTCTCGATTAAACATCTTTCATCGCGCTGCTCTG	284						
QY	378	TGCTGTATTGTTCTTTGGTTCATCTTTTGGAGAGAAATAGATGAGTGAACGAATCCATCAC	437						
Db	285	CAGCTGCAATGTTCATCGGCCACTTCTCGAAGGGAACCGATGGGTGAACGAGTCCATCAC	344						
QY	438	CGCCTTGTGATGGGCTAGGCACCTGGGTGTTACCAATTTTGTGATTAGTAAAGGAAAAAG	497						
Db	345	CGCGCTGTGATGGGCTCATCACCGAGGGCTCATCTGCTGGTACTTAATGGGACAAA	404						
QY	498	CTCGCATCTTCTCGCTTTAGTGAAGATCTTTCTTCATATATCTTTTGGCCACCCATTAT	557						
Db	405	CTCAGGCATTCTTGTGTTTCAGCGAGGACCTGTGTTTTCATATATTTTACTTCGCGCGATAAT	464						
QY	558	ATTCAATGCAAGGTTTCAAGTAAAAAGAACGAGTTTTTTCGCAATTTTCGTGACTATTAT	617						
Db	465	CTTCAATGCCGGTTCAGTAAAGAAAGCAATTTCTTCGCACTTTTAAACGATTAT	524						
QY	618	GCTTTTGGTGTCTGTGGGACTATTATTTCTTGGCAATCATATCTCTAGGTGTAAACA	677						
Db	525	TTTGTGTTGGTGTATTTGGGACTCTGATTTCTTGTGTAATAATCTCTCTGGTGTATGGG	584						
QY	678	GTCTTTAAGAGTTGGACATTTGGAACCTTTGACTTTGGGTGATATCTTGTCTATTGGTGC	737						
Db	585	GTGTTTCAAGAACTTGATGTGTGTCCTACTCGAGCTTGGGACTATCTTGCAATTTGGTGC	644						
QY	738	CATATTTGCTGCAACAGATTCAATGATGTACACTGCAGGTTCTGATCAAGACGAGACACC	797						
Db	645	TATTTTCTCGGCAACAGATTCTGTTTGCACTTACAGGTGCTTAAACAGGATGAACACC	704						
QY	798	TTTGCTTTACAGTCTTGTATTTCGAGAGGGTGTGTTGAATGATGCAACGTCAGTTGTGGT	857						
Db	705	CCTACTCTATAGTCTAGTTTGTGGTGAAGGTGTTGTTAATGATGCCACATCTGTTGTGCT	764						
QY	858	CTTCAACGGATTTCAGAGCTTTGATCTCACTCACTCAACCAACGAGCTGCTTTTCATCT	917						
Db	765	CTTCAATGCAATTGAAACCTTGATATTGATAATTTTGTATGCTATTGTTCTGTTGAATTT	824						
QY	918	TCTTGGAACTCTTGTATTGTTTCTCTAAGTACCTTGTGTTGCTGTCGCAACCGGTCT	977						
Db	825	CGTCGGAAATTTCTCTACTTGTCTTCCACAGACCACTACTTGGAGTAGTACTACCGGGTT	884						
QY	978	GATAAGTGTGATGTTATCAAGAAGCTATATCTTTGGAAGGCACTCAACTGACCGAGAGGT	1037						
Db	885	GCTTAGTGATACATATATCAAGAGCTCTGTTTTCGACAGATTCACATGATAGAGAAGT	944						
QY	1038	TGCCCTTATGATGCTTATGGCGTATCTTCTTATATGCTTGTGAGCTTTTTCGACTTGAG	1097						
Db	945	TTCTATCATGATFACTCATGGCATACTTTTCATACATGATATCAATGCTGTTGGACCTGAG	1004						
QY	1098	CGGTATCCTCACTGTGTTTCTGTTGGTATTGTTGATGTCCTTACATGATGATGATGATG	1157						
Db	1005	TGGAATTTCTACTGCTTCTTCTGTTGGAATAGTAAATGTCACATTAACCTTGGCATAATGT	1064						
QY	1158	AACGGAGAGCTCAAGAAATAACAAGCATACCTTTTGCAACTTTTGTCAITTTCTTGCGGA	1217						
Db	1065	GACAGAAAGTCTAGGGTTTACCACCAAGCATACTTTTGCACATTTTCAATTCATTGTCAGA	1124						
QY	1218	GACATTTATTTCTGTATGTTGGAATGATGCTTGGACATTTGACAAAGTGGAGATCCGT	1277						
Db	1125	AATTTTTCCTTCTCTATGTTGGGATGGATGCAATTGGACATTGAGAAGTGGAAATTTAGC	1184						
QY	1278	GAGTGACACACCGGGAACATCGATCGC-AGTGAGCTCAATCCTAATGGTCTGTGTCATGG	1336						
Db	1185	TAGTAGCAGTCTTAAGAAACCAATTTGCGTTTAAAGTGCATTTATTTTGGGCTTGGTTAAG	1244						
QY	1337	TTGGAAGAGCAGCGTTTCGTTCTTTCGCTTATCGTTTCTATCTAACTTACGCCAAGAGAAATC	1396						

1245	TTGGAAGAGCGGCATTTGTTATTTCCCTTTTGTGTTCTTATCCAACTTAAAGCAAAAAGGAGG	1304	
QY	1397	AAAGCGAGAAATCAACTTTAAACATGCAAGGTTTGATTTGGTGTCTGTTCTCATGAGAG	1456
Db	1305	CCCGTCCAAAGATCTCCTTCAAGCAACAAGTAATCATATGTTGGGCTGGTCTCATGAGAG	1364
QY	1457	GTGCTGTATCTATGGCTCTTGCATACACAAAGTTTCAAGGGCCGGGCGACACATGTATC	1516
Db	1365	GAGCAGTGTCAATTTGCGCTTATACAAAGTTTACAGCATCTGGTCCACTGAAGTGC	1424
QY	1517	GCAGGAATGCAATCATGATCACGAGTACGATAAATCTGTCTCTTTTGTAGCACAGTGGTGT	1576
Db	1425	GAGTCAATGCTATCATGATCACGACAGATTAATTTGTTGTTCTATTTCAGCAATGGTTT	1484
QY	1577	TTGATGCTGACCAAAACCACTCATTAAGCTACCTATTACCGCACAGAAACCCACCGA	1636
Db	1485	TCGGCTCTGTCAGCAAGCGCTGCTCATCTCTCATCCAC-CAAGGACTGGACTGAAC	1543
QY	1637	GCATGTTATCTGATGACACACACCCCAAAATCCATACATATCCCTTTGTTGGACCAAGACT	1696
Db	1544	ACGTGCTCTCTGCTCTCAAGCAGTCTATGCTGGACCCACTCTTACTAGCATGA-----	1598
QY	1697	CGTTCAATTGAGCCTTCAGGGAAACCAAAATGTGCTCGGCTCGACATATACGTGGCTTCT	1756
Db	1599	TGGGCTCTGATTTGATGTAGGCGAGATCAACTCCCTCAATACACCTCCAGTTCATTC	1658
QY	1757	TGACACGCGCCACTCGAACCGTGTGATTAATCTACTCGAGACAAATTTGATGATCTCTTCATGC	1816
Db	1659	TCACCGGCGGAGCTGCTGCTCCATCGCTTTGGCGCAAGTTTGGAGATCGGTTTCATGC	1718
QY	1817	GACCGCTCTTTGGAGGCTGCTGGCTTTGTACCTTTTTCAGGTTTCCCACTCAGAGAA	1876
Db	1719	GCCGCTGTTTCGGGGGGGAGGTTTCGTCCTTTTGCTGCTGGTTCGCCGTGGAGAGGA	1778
QY	1877	ACCTCTCTGA 1886	
Db	1779	GTGTCCTCTGA 1788	

RESULT 2									
AY109416									
LOCUS	Zea mays	CL694_1	mRNA	linear	HTC	17-OCT-2002			
DEFINITION	3272 bp mRNA sequence.								
ACCESSION	AY109416								
VERSION	AY109416.1	GI:21213132							
KEYWORDS	HTC.								
SOURCE	Zea mays								
ORGANISM	Zea mays								
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.									
REFERENCE	1	(bases 1 to 3272)							
AUTHORS	Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.								
Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes									
JOURNAL	Unpublished (2002)								
REFERENCE	2	(bases 1 to 3272)							
AUTHORS	Coe,E.H.								
TITLE	Direct Submission								
JOURNAL	Submitted (25-APR-2002)	Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA							
If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.									
Location/Qualifiers									
FEATURES	1..3272								
source	/organism="Zea mays"								
	/mol_type="mRNA"								

ORIGIN

RESULT 3
C99909
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

[illegible]

```
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 651)
AUTHORS Motohashi, R., Shinozaki, K. and Yamaguchi-Shinozaki, K.
TITLE Arabidopsis thaliana YAC C1C3B1 region specific cDNA, clone 2
JOURNAL Unpublished (1999)
COMMENT Contact: Motohashi R
Laboratory of Plant Molecular Biology
Institute of Physical and Chemical Research (RIKEN)
3-1-1, Koyadai, Tsukuba 305-0074, Japan
Tel: +81-298-36-4359
Email: motohashi@rtc.riken.go.jp.

FEATURES             source
    source
    1..651
        /organism="Arabidopsis thaliana"
        /mol_type="mRNA"
        /db_xref="taxon:3702"
        /clone="65"
    /clone_lib="Arabidopsis thaliana library (Motohashi R)"

ORIGIN
Query Match      27.3%; Score 595.6; DB 6; Length 651;
Best Local Similarity 98.2%; Pred. No. 8e-131;
Matches 640; Conservative 4; Mismatches 3; Indels 5; Gaps 4;

QY 1225 ATTTCTTTGTATGTTGGAAATGATGCCCTTGGACATATGACAAAGTGAGATCCGTGATGAC 1284
DB 1 ATTTCTTTGTATGTTGGAAATGATGCCCTTGGACATATGACAAAGTGAGATCCGTGATGAC 60

QY 1285 ACACCGGGAACATCGATCGCAGTAGCTCAATCCTTAATGGTCTGGTCATGTTGGAGA 1344
DB 61 ACACCGGGAACATCGATCGCAGTAGCTCAATCCTTAATGGTCTGGTCATGTTGGAGA 120

QY 1345 GCAGGGTTCGTCTTTCGGTTATCGTTTCTATCTAATTTAGCCAAAGAAATCAAGCGAG 1404
DB 121 GCAGGGTTCGTCTTTCGGTTATCGTTTCTATCTAATTTAGCCAAAGAAATCAAGCGAG 180

QY 1405 AAAATCAACTTTAATCAATGATGTTGGTGTCTGTTCTCATGAGAGGTGCTGTA 1464
DB 181 AAAATCAACTTTAATCAATGATGTTGGTGTCTGTTCTCATGAGAGGTGCTGTA 240

QY 1465 TCTATGGCTCTTGCATACAAACAGTTTACAGGGCCGGGCACACAGATGTACGGGAAAT 1524
DB 241 TCTATGGCTCTTGCATACAAACAGTTTACAGGGCCGGGCACACAGATGTACGGGAAAT 300

QY 1525 GCAATCATGATCAGAGTACGATACTGTCTGTCTTTTGTAGCACAGTGGTGTGTTGATG 1584
DB 301 GCAATCATGATCAGAGTACGATACTGTCTGTCTTTTGTAGCACAGTGGTGTGTTGATG 360

QY 1585 CTGACCAAAACCACTCATAAGCTTACCTATTATCGCACCAAGACCGCCACACGAGCATGTTA 1644
DB 361 CTGACCAAAACCACTCATAAGCTTACCTATTATCGCACCAAGACCGCCACACGAGCATGTTA 420

QY 1645 TCTGATGACAAACACCCCAAAATCCATACATATCCCTTTGTTGGACCAAGACTCGTTCAAT 1704
DB 421 TCTGATGACAAACACCCCAAAATCCATACATATCCCTTTGTTGGACCAAGAC -CGTTCAAT 479

QY 1705 GAGCCTTCAGGGAACCAATGTGCTCGGCTGACAGTATACGTGGCTCTTGACACGG 1764
DB 480 GAGCCTTCAGGGAACCAATGTGCTCGGCTGACAGTATACGTGGCTCTTGACACGG 539

QY 1765 CCCACTGAACCGGTGATTTACTACT - GGAGACAAATTTGATGATCTCTTTCATCGCACCGGT 1823
DB 540 CCCACTGAACCGGTGATTTACTACTTCTGCGGAGACAAATTTGATGATCTCTTTCATCGCACCGGT 599

QY 1824 CTTT -GGAGGTGCTGGCTTTGACCTTTGTT -CCAGGTTCTCAACTGAG 1872
DB 600 CTTTGGAGGTGCTGGCTTTGACCTTTGTTTTCARGGTTTCTCAACTGAG 651

RESULT 4
```

```
CA767092
LOCUS AF53-Rpf_13_p08_T7_032.ab1 IRRI Drought Stress Panicle Library
DEFINITION Oryza sativa (indica cultivar-group) cDNA clone C0004976 5', similar
to Sodium/hydrogen exchanger 6 (Na(+)/H(+) exchanger 6) (NHE-6),
mRNA sequence.
CA767092
ACCESSION CA767092.2 GI:27549114
VERSION EST.
KEYWORDS Oryza sativa (indica cultivar-group)
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Euhartoidae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 834)
AUTHORS Bennett, J., Arumugam, K., Lafitte, R., Wen, J., Rudd, S. and
Bruskiewicz, R.M.
TITLE IRRI Drought Stress Panicle cDNA Library
JOURNAL Unpublished (2002)
COMMENT On Dec 2, 2002 this sequence version replaced gi:25996347.
Contact: Richard Bruskiewicz
Biometrics and Bioinformatics Unit
International Rice Research Institute
DAPO 7777, Metro Manila, Philippines
Tel: +63-2-845-0563
Fax: +63-2-845-0606
Email: r.bruskiewicz@cgiar.org
International Rice Information System (IRIS)
http://www.iris.irri.org: D0204975
Assignment of putative function to the sequence by S. Rudd of the
Munich Information Center for Protein Sequences
(http://mips.gsf.de)
Plate: 13 row: P column: 08.

FEATURES             source
    source
    1..834
        /organism="Oryza sativa (indica cultivar-group)"
        /mol_type="mRNA"
        /cultivar="IR64"
        /db_xref="taxon:39946"
        /clone="C0004976"
        /tissue_type="Panicles"
        /dev_stage="flowering"
        /clone_lib="IRRI Drought Stress Panicle Library"
        /note="vector: pBluescript II SK+; Water stress was
        applied by not watering for 4 consecutive days. Panicles
        were collected from control (well watered) and stressed
        plants at 2 days before heading, at heading, 50% flowering
        and 4 days after 50% flowering."

ORIGIN
Query Match      22.4%; Score 487.2; DB 6; Length 834;
Best Local Similarity 73.9%; Pred. No. 5.6e-105;
Matches 615; Conservative 0; Mismatches 217; Indels 0; Gaps 0;

QY 760 GTATGTACATCGCAGGTTCTGAATCAAGAGAGACACCTTGCTTTCAGCTCTGTATTC 819
DB 2 GTCTGCACATGCGAGGTCCTCAATCAGATGAGACACCTTTTGTACAGTCTGTATTC 61

QY 820 GGAGAGGCTGTGTGAATGATGCAACGTCAGTTGTGCTTCAACGGGATTCAGAGCTTT 879
DB 62 GGTGAAGGTGTGTGAACGATGCTACATCAATTGTGCTTTTCAACGACATACAGACTTT 121

QY 880 GATCTCACTACCTAAACACGAAAGCTGCTTTTCATCTTCTTGAAACTTCTTGATTTG 939
DB 122 GATCTGTCCACATAGATGGGCTGTGCTTCTGAAATTTCTTGGGAACTTCTTTATTTA 181

QY 940 TTTCTCTAGTACCTTGTGCTGCAACCGTCTGTAAGTGGTATGTTATCAAG 999
DB 182 TTTTGTGAGACACCTTCTTGGAGTATTTGCTGGATTTGCTAGTGATACATATCAAG 241

QY 1000 AAGCTATACCTTTTGAAGGCACTCAACTGACGAGAGGTTGCCCTTATGATCTTATGCG 1059
DB 242 AAGCTATACATTTGAAGGCACTTCTACTGACCGTGAGGTTGCCCTTATGATCTATGGCT 301
```

```
QY 1060 TATCTTCTTATATGCTTCTGAGCTTTTCGACTTGGAGCGGTATCTCAGTGTGTTTTT 1119
    |||||
Db 302 TACCTTTTATATATGCTTCTGAGTTGTAGATTTTGGCGGCAATCTCACCGTATCTTTC 361
    |||||
QY 1120 TGTGGTATTTGATGCTCCATTTACACATGGGCAATGTAAACGAGAGCTCAAGAAATACA 1179
    |||||
Db 362 TGTGGTATTTGATGCTCCATTTACACATGGGCAATGTAAACGAGAGCTCAAGAGTTACA 421
    |||||
QY 1180 ACAAGACATACCTTTGCACTTTGTCATTTCTTGGGAGACATTTATTTTCTGTATGTT 1239
    |||||
Db 422 ACAAGACATACCTTTGCACTTTGTCATTTCTTGGGAGACATTTATTTTCTGTATGTT 481
    |||||
QY 1240 GGAATGGATGCTTTGGACATTTGCAAGTGGAGATCCGTGAGTGAACACACCGGGAACATCG 1299
    |||||
Db 482 GGGATGGATGCTTTGGACATTTGCAAGTGGAGATTTGCCAGTGAACACACCGGGAACATCC 541
    |||||
QY 1300 ATGCGAGTGAAGTCAATCTTAATGGGTCTGGTCAATGGTGGAGAGAGCGGTTCGTCTTT 1359
    |||||
Db 542 ATGGGATAAGCTCAATTTTGTAGGATTTGCTTGTCTGGAGAGCTGCTTTTGTATTC 601
    |||||
QY 1360 CGGTATCTCTTCTATCACTTATCAAGTGAAGATCAAGCGAGAAATCACTTTAATC 1419
    |||||
Db 602 CGCTGTCTCTTGTGAACTTATCAAGAAAGGACCGAATGAAGAAATTAACCTGGAGA 661
    |||||
QY 1420 ATGCAAGTGTGATTTGGTGTCTGCTCTCATGAGAGGTGCTGTATCTATGGCTCTTGCA 1479
    |||||
Db 662 CAGCAAGTGTGATTTGGTGTCTGCTCTCATGAGAGGTGCTGTATCTATGGCTCTTGCT 721
    |||||
QY 1480 TACAACAGATTTTACAAGGCGCGGACACAGATGTACCGGGAATGCAATCATGATCAG 1539
    |||||
Db 722 TACAATAAGTTTACAAGATCTGGCCATCTAGCTTTCACGGCAATGCAATATGATCACC 781
    |||||
QY 1540 AGTACGATTAACGTCTGCTCTTTTACGACAGTGTGTTGGTATCTCTGACCA 1591
    |||||
Db 782 AGCACCATCACTGCGCTCTTTTACGACATGATGGTATTTGGGATGATGACAA 833
    |||||
```

RESULT 5

```
LOCUS CL973674
DEFINITION OsIRCC024729 Oryza sativa Express Library Oryza sativa (indica
cultivar-group) genomic, genomic survey sequence.
ACCESSION CL973674
VERSION CL973674.1 GI:52401874
KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
REFERENCE 1 (bases 1 to 1449)
AUTHORS Ma,L., Wang,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
Wong,G.K.S., Deng,X.W. and Wang,J.
TITLE An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
JOURNAL Unpublished (2004)
COMMENT Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
FEATURES
Location/Qualifiers
1..1449
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
```

/note="Oryza sativa exon trapped genomic sequences"

```
ORIGIN
Query Match 22.0%; Score 478.8; DB 9; Length 1449;
Best Local Similarity 60.4%; Pred. No. 6.2e-103;
Matches 948; Conservative 0; Mismatches 457; Indels 165; Gaps 3;
QY 312 GCCTTCGTTATCGACATCTGATCAGCTTCGTGCTGCGTTCCTATCAACCTGTTGTCGGCT 371
    |||||
Db 33 GGCTCTGTACAGGACCTCGACTAGCGTTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 92
    |||||
QY 372 TCTTTGTGCTTGTATTTGTTCTTGTGTCATCTTTTGGAGAGAAATAGATGGAAGCAATC 431
    |||||
Db 93 GCTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 152
    |||||
QY 432 CATCACCGCTTGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 491
    |||||
Db 153 CATCACCGCTTGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 212
    |||||
QY 492 AAAAAGCTCGCATCTTCTGCTCTTTAGTGAAGATCTTTTCTTCTATATATCTTTTCCACC 551
    |||||
Db 213 GAAGAGCTCGCATTTATTTGCTCTTCTGAGTGAAGATCTTCTTCTATCTACCTCCTCCTCC 272
    |||||
QY 552 CATTATATCAATGAGGCTTCAAGTAAAAAAGAGCAGTTTTCGCAATTTTCGTGAC 611
    |||||
Db 273 GATCATCTTCAATGAGGCTTCTGCTCTAGAGTTCTACTCTTGGTCCATTTAC----- 327
    |||||
QY 612 TATTATGCTTTTGTGCTGTTGGGACTATTATTCTTCTGCAATCATATCTCTAGGTGT 671
    |||||
Db 328 -----AGTGCTGC 335
    |||||
QY 672 AACACAGTTCTTTAAGAGTTGGACATTTGGAACCTTTGACTTTGGGTGATTTATCTTGCTAT 731
    |||||
Db 336 CATTGCAATATTCAGCAATGAAATTTGGAACGCTGATGTAGAGAGATTTCTTCTGCAAT 395
    |||||
QY 732 TGGTGCCATATTTGCTGCAACAGATTCAGTATGTACACTGCAAGTTCGAAATCAAGACGA 791
    |||||
Db 396 TGGAGCCATCTTTCTGGACAGATTTCTGCTGACATTTGCAGGTCCTCAATCAGGATGA 455
    |||||
QY 792 GACACCTTTGCTTACAGTCTTTGATTTCCGAGAGGTTGTTGATGATGCACTCAGT 851
    |||||
Db 456 GACACCTTTTGTGACAGTCTGCTGTTTCCGTTGGAAGGTTGTTGGAACGATGCTACATCAAT 515
    |||||
QY 852 TGTGCTCTTCAACGCGATTCAGAGCTTTGATCTCACTCACCTAAACACGAGCTGCTTT 911
    |||||
Db 516 TGTGCTTTTCAACGCGACTACAGAACTTTGATCTTGTCCACATAGATGCGGCTGCTGCTCT 575
    |||||
QY 912 TCATCTTCTTGGAAACTTCTTGTATTTGTTTCTCCTAAGTACCTTTGCTGCTGCTGCTGCTAAC 971
    |||||
Db 576 GAAATTTCTTGGGAACTTCTTTTATTTATTTTGTGCGAGCACCTTCTTCTTGGAGTATTTGC 635
    |||||
QY 972 CGGTCTGATAGTGGGTATGTTTCAAGAACTATCTTCAAGAGGCTCACTCACTGACCG 1031
    |||||
Db 636 TGGATTTGCTCAGTGCATACATAATCAAGAACTATACATTTGGAAGGCAATCTTACTGACCG 695
    |||||
QY 1032 AGAGTTTCCCTTATGATGCTTATGGCTATCTTTCTTATATGCTGCTGAGCTTTTCTGA 1091
    |||||
Db 696 TGAGTTTCCCTTATGATGCTCTGCTGCTTACCTTTTATATATGCTGCTGCTGCTGCTAGA 755
    |||||
QY 1092 CTTGAGCGGTATCCTCAGTGTGTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1151
    |||||
Db 756 TTTGAGCGGCTTCTCAGCGTATTTCTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 815
    |||||
QY 1152 CAATGTAACGAGAGCTCAAGAAATCAACAAAGCATACCTTTTGCACCTTTGTCATTTCT 1211
    |||||
Db 816 TAACGTCAACAGAGATTTCAAGAGTTTACAAACAA----- 848
    |||||
QY 1212 TGGGAGACATTTATTTTCTTGTATGTTGGAATGGAATGCTTGGACATTTGACAAGTGGAG 1271
    |||||
Db 849 ----- 848
    |||||
QY 1272 ATCGTGAGTGACACACCGGGAACATCGATCGCAGTGAAGCTCAATCTTAATGGGTCTGGT 1331
    |||||
```


FEATURES
SOURCE

ORIGIN

RESULT 8	AV792419	433 bp	mrna	linear	EST 29-MAR-2002
LOCUS	AV792419	RAFL7 Arabidopsis thaliana cDNA clone RAFL07-14-P04 3',			
DEFINITION	mrna sequence.				
ACCESSION	AV792419				
VERSION	AV792419.1	GI:19826402			
KEYWORDS	EST.				
SOURCE	Arabidopsis thaliana (thale cress)				
ORGANISM	Arabidopsis thaliana				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
REFERENCE	1 (bases 1 to 433)				
AUTHORS	Seki,M., Narueaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.				
TITLE	Large scale analysis of Arabidopsis full-length cDNA (2002b)				
JOURNAL	Unpublished (2002)				
COMMENT	Contact: Motoaki Seki Plant Functional Genomics Research Group RIKEN Genomic Sciences Center 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan Tel: 81-298-36-4359 Fax: 81-298-36-9060 Email: mseki@tc.riken.go.jp An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified Bluescript vector. Please visit our web				

site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES

source Location/Qualifiers
 1..433
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /db_xref="taxon:3702"
 /clone="RAFL07-14-P04"
 /dev_stage="rosette plants"
 /lab_host="DH10B"
 /clone_lib="RAFL7"
 /note="Site 1: BamHI; Site 2: SalI; subjected to cold-treated (1, 2, 5, 10, 24 hr)"

ORIGIN

Query Match 19.8%; Score 432; DB 1; Length 433;
 Best Local Similarity 100.0%; Pred. No. 7.2e-92;
 Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1718 ACCAATGTGCTGGCTGACAGTATACGTGGCTTTTGACAGCGCCCACTCGAACCG 1777
 Db 433 ACCAATGTGCTGGCTGACAGTATACGTGGCTTTTGACAGCGCCCACTCGAACCG 374
 QY 1778 TGCATTACTCTGGAGACAAATTGATGACTCTTCATCGACCCGCTCTTTGGAGTCTGT 1837
 Db 373 TGCATTACTCTGGAGACAAATTGATGACTCTTCATCGACCCGCTCTTTGGAGTCTGT 314
 QY 1838 GCTTTGTACCTTTCTCCAGGTTCTCCAGTCTCGAGAGAACCTCTCGATCTTAGTAAGG 1897
 Db 313 GCTTTGTACCTTTCTCCAGGTTCTCCAGTCTCGAGAGAACCTCTCGATCTTAGTAAGG 254
 QY 1898 CTTGAGGTAACGTGGAGAAAGCTTTGATTTTGTGAGAAAGGGTGATTCAAAT 1957
 Db 253 CTTGAGGTAACGTGGAGAAAGCTTTGATTTTGTGAGAAAGGGTGATTCAAAT 194
 QY 1958 TATGCTTTGTGTAATTAATCATTTGTAATATCTTTGTGAGGACAGAAATCTGTCTTA 2017
 Db 193 TATGCTTTGTGTAATTAATCATTTGTAATATCTTTGTGAGGACAGAAATCTGTCTTA 134
 QY 2018 ACGTTTTCAGACGAGAAAGCAAAACATGCGCACTTTGAAAGTGTGATGATGTAATG 2077
 Db 133 ACGTTTTCAGACGAGAAAGCAAAACATGCGCACTTTGAAAGTGTGATGATGTAATG 74
 QY 2078 TTATATTATATTTTGTGTTGTTGTAACCAACTACATTTGTTTATGTTTGAATTTG 2137
 Db 73 TTATATTATATTTTGTGTTGTTGTAACCAACTACATTTGTTTATGTTTGAATTTG 14
 QY 2138 GTTTTGTCTTCG 2149
 Db 13 GTTTTGTCTTCG 2

RESULT 9

AV825792
 LOCUS AV825792 RAFL7 Arabidopsis thaliana cdna clone RAFL07-14-P04 5',
 DEFINITION mRNA sequence.
 ACCESSION AV825792
 VERSION AV825792.1 GI:19867852
 KEYWORDS EST.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shingawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.
 TITLE Large scale analysis of Arabidopsis full-length cdna (2002b)
 JOURNAL Unpublished (2002)
 COMMENT Contact: Motoaki Seki

Plant Functional Genomics Research Group

RIKEN Genomic Sciences Center

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel: 81-298-36-4359

Fax: 81-298-36-4359

Email: meeki@rtc.riken.go.jp

An Arabidopsis full-length cdna library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLIC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES

Location/Qualifiers

1..629
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /db_xref="taxon:3702"
 /clone="RAFL07-14-P04"
 /dev_stage="rosette plants"
 /lab_host="DH10B"
 /clone_lib="RAFL7"
 /note="Site 1: BamHI; Site 2: SalI; subjected to cold-treated (1, 2, 5, 10, 24 hr)"

ORIGIN

Query Match 19.7%; Score 429.4; DB 1; Length 629;
 Best Local Similarity 98.0%; Pred. No. 3.2e-91;
 Matches 433; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1 CCTCTCTGTTTCGTTCTCGTAGCAGAGAGAGAAAGAAATCTCAGGTTTTAGCTTTTCCA 60
 Db 187 CCTCTCTGTTTCGTTCTCGTAGCAGAGAGAGAGAAATCTCAGGTTTTAGCTTTTCCA 246
 QY 61 AGCTTCCAAATTTTGAATTTTGATCTTCTGGGCTCTTTTGTAAATCAGACTGAAGATAT 120
 Db 247 AGCTTCCAAATTTTGAATTTTGATCTTCTGGGCTCTTTTGTAAATCAGACTGAAGATAT 306
 QY 121 TTAGATTACCCAGAAAGTTGTTCAAGGAATGGTTTTCAGTGACAGCAGCGAAGATAAAG 180
 Db 307 TTAGATTACCCAGAAAGTTGTTCAAGGAATGGTTTTCAGTGACAGCAGCGAAGATAAAG 366
 QY 181 AGACTTTTTCAGATTTTGTCTGATCCAAATCTCAATAGTTGTTTCATCTCTTGAT 240
 Db 367 AGACTTTTTCAGATTTTGTCTGATCCAAATCTCAATAGTTGTTTCATCTCTTGAT 426
 QY 241 CAAATCTGGAAGAGGAAAGTTTGTGGATCTAGAGAGAGATAACAATTTGGATTCTCTA 300
 Db 427 CAAATCTGGAAGAGGAAAGTTTGTGGATCTAGAGAGAGATAACAATTTGGATTCTCTA 486
 QY 301 GTGTCGAAACTGCTTCGTTATCGACATCTGATCACGCTTCTGTGGTTGCGTTGAATCTC 360
 Db 487 GTGTCGAAACTGCTTCGTTATCGACATCTGATCACGCTTCTGTGGTTGCGTTGAATCTC 546
 QY 361 TTTGTCGACTTCTTTGTCGCTTGTATTTGTTCTTCTGTCATCTTTTGGAGAGAGATAGATGG 420
 Db 547 TTTGTCGACTTCTTTGTCGCTTGTATTTGTTCTTCTGTCATCTTTTGGAGAGAGATAGATGG 606
 QY 421 ATGAACGAATCCATCACCGCT 442
 Db 607 GTGAACGAATCCATCACCGCT 628

RESULT 10

CD531888
 LOCUS CD531888
 DEFINITION 12022 Arabidopsis Leaf Senescence Library Arabidopsis thaliana cdna
 3', mRNA sequence.
 ACCESSION CD531888
 VERSION CD531888.1 GI:40451900
 KEYWORDS EST.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eutrosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 448)
Guo, Y., Cai, Z. and Gan, S.
Transcriptome of Arabidopsis leaf senescence
Plant Cell Environ. 27 (5), 521-549 (2004)
Contact: Susheng Gan
Department of Horticulture
Cornell University
119 Plant Science, Cornell University, Ithaca, NY 14853-5904, USA
Tel: 607 254 5418
Fax: 607 255 0599
Email: sg288@cornell.edu
Insert Length: 448 Std Error: 0.00
Seq primer: T7
POLYA=Yes.

FEATURES

source Location/Qualifiers
1..448
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecotype="Landsberg erecta"
/db_xref="taxon:3702"
/cissue_type="leaf"
/dev_stage="yellow Leaf With Greenish Base Area"
/lab_host="E. coli"
/clone_lib="Arabidopsis Leaf Senescence Library"
/note="Organ: Rosette Leaf; Vector: pBluscript SKII+;
Site 1: EcoRI; Site 2: EcoRI; Senescent rosette leaves #5
and #6 (counted from the bottom) were harvested and
immediately frozen in liquid N2. The leaves were visibly
yellow excepted for the leaf base areas that were still
greenish."

ORIGIN

Query Match 19.4%; Score 422.4; DB 6; Length 448;
Best Local Similarity 99.3%; Pred. No. 1.4e-89;
Matches 445; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
1615 CGCACCAGACGCCACGAGCATGTTATCTGATGACAACCCCAATCCATACAT 1674
Db 1 CGCACCAGACGCCACGAGCATGTTATCTGATGACAACCCCAATCCATACAT 60
1675 ATCCCTTTT-GTTGGACCAAGACTCGTTTCATTGAGCCTTCAGGGAACCAATGTGCTCG 1733
Db 61 ATCCCTTTGTTGGACCAAGACTCGTTTCATTGAGCCTTCAGGGAACCAATGTGCTCG 120
1734 GCGTGACATATACGTGGCTTTTGACACGGCCCACTCGAACCGTGCAATTACTGGAG 1793
Db 121 GCGTGACATATACGTGGCTTTTGACACGGCCCACTCGAACCGTGCAATTACTGGAG 180
1794 ACATTTTGATGACTCCTTCATGGCAGCCGCTCTTTGAGGTGCTGGCTTTGTACCCCTTGT 1853
Db 181 ACATTTTGATGACTCCTTCATGGCAGCCGCTCTTTGAGGTGCTGGCTTTGTACCCCTTGT 240
1854 TCAGGTTCTCCAACTGAGAGAAACCTCTGATCTTACTAGGCTTTAGGTTAGCGTGG 1913
Db 241 TCAGGTTCTCCAACTGAGAGAAACCTCTGATCTTACTAGGCTTTAGGTTAGCGTGG 300
1914 AAGAAAAGCTTTGA-TTTTTTTGGTAGAAAAGGGTGATTCAAATATATCTTTTGTGTAA 1972
Db 301 AAGAAAAGCTTTGATTTTTTTTTGGTAGAAAAGGGTGATTCAAATATATCTTTTGTGTAA 360
1973 ATTATCCATTGTAAATATTGTTTGTGAGGACAGAAATCTGCTTAACGTTTTGAGAGCAG 2032
Db 361 ATTATCCATTGTAAATATTGTTTGTGAGGACAGAAATCTGCTTAACGTTTTGAGAGCAG 420
2033 AAGCAAAACATGGCAACTTTGAAGTGT 2060
Db 421 AAGCAAAACATGGCAACTTTGAAGTGT 448

RESULT 11

BU004460
LOCUS
DEFINITION

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

FEATURES
source

BU004460 733 bp mRNA linear EST 22-AUG-2002
QG55E06.yg.abi OG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
QG55E06, mRNA sequence.
BU004460
VERSION
KEYWORDS
SOURCE
ORGANISM
Lactuca sativa
Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
1 (bases 1 to 733)
Kozik, A., Micheltore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,
Elison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Micheltore]
Department of Vegetable Crops, R.W.Micheltore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.org [micheltore@vegmail.ucdavis.edu]
belongs to contig OG_CA_Contig6585, see http://cgpdb.ucdavis.edu/
for details.
Plate: QGGS row: E column: 06.
Location/Qualifiers
1..733
/organism="Lactuca sativa"
/mol_type="mRNA"
/cultivar="L.serriola"
/db_xref="taxon:4236"
/clone="QG55E06"
/lab_host="E.coli"
/clone_lib="OG_EFGHJ lettuce serriola"
/note="Vector: pBRCDNA51AB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgpdb.ucdavis.edu/
TAG_TISSUE=flowers environmental stress
TAG_LIB=OG_EFGHJ lettuce serriola
TAG_SEQ=CGAATGCGGG"

ORIGIN

Query Match 19.1%; Score 416.6; DB 5; Length 733;
Best Local Similarity 75.4%; Pred. No. 3.7e-88;
Matches 518; Conservative 0; Mismatches 169; Indels 0; Gaps 0;
323 CGACATCTGATCACGCTTCTGTGGTTGGTGGAAATCTCTTTTGGCACTCTTTGTGCTT 382
Db 47 CTACCTCTGAGTACTCTTCCATTTGCTCTATGAACCTGTTTGTCTCTCTTCTTGTGCTT 106
383 GTATTGTTCTTGGTCATCTTTTGGAGAGATAGATGATGAACCAATCCATCCAGCTT 442
Db 107 GTATCGTAATCGGTCTATCTTTTGGAGAGAAATCGATGATGAACCAATCTATCTAC 166
443 TGTTCATTGGGCTAGGCCTGGTGTATACATTTTCTTCAATAGTAAAGAAAAAGCTGCG 502
Db 167 TGTTCATTGGTATTTGCACTGGAGTTGTTATTTTGAAGCAGTGGAGAACAAATTCAC 226
503 ATCTTCTCGTCTTTAGTGAAGATCTTTTCTTCATATATCTTTTGGCCACCCCAATATATCA 562
Db 227 ATCTTCTAGTCTTTCAGTGAAGATCTTTTCTTCATTTATCTTCTTCCACTATCATCTTCA 286

Qy	563	ATGAGGGTTTCAAGTAAAAAAGACGAGTTTTTCCGCAATTTCTGTGACTATTATGCTTTT	622
Db	287	ATGCTGGGTTTCAGGTTAAGAAGAAACAATTTTTTCGCAATTTCTAGACCATTTGTGCTAT	346
Qy	623	TTGGTGCTGTTGGGACTATTATTTCTTGCACAATCATATCTCTAGGTGTAAACACAGTTCT	682
Db	347	TTGGTGCTGTTGGCACTGTGATATCTTTCCACCATCATATCATTTGGTGCTATAAATTT	406
Qy	683	TTAAGAGTTGGACATTCGGAACCTTTGACTTGGGTGATTAATCTTCTATTTGGTGCCATAT	742
Db	407	TCCAAAGGATGGATGTTGGTACCTTTGAGCTTTGGAGACTTCTTCGCAATTTGGTGCATAT	466
Qy	743	TTGCTGCAACGATTTCAGTATGTACACTGCAGTTTCTGAAATCAAGACGAGACACCTTTGC	802
Db	467	TTTCAGCCACCAGATCCCGTTTGCACTTTTGCAGGTGTGAAATCAGGATCAGACACCTTTAT	526
Qy	803	TTTACAGTCTTGATTTCGGAGAGGGTGTGTGAAATGATGCAACGTCAGTTGTGGTCTTCA	862
Db	527	TATATAGTTGGTGTTTGGTGAAGGTGTGGTGAATGATGCCACATCAGTTGTGCATCTTCA	586
Qy	863	ACGCGATTTCAGAGCTTTTGATCTCACTCACTAAACCAGAGCTGCTTTTCATCTTCTTG	922
Db	587	ATGCAGTTTCAAACTTTTGATCTCTCTCAAAATCACAACGCTGTGTGCATTTTCACTGATTG	646
Qy	923	GAAACTTCTTGATTTGTTTCTCCTAAGTACCTTGCTTGGTGCTGCGAACCGGTCTGATAA	982
Db	647	GAATTTCTTTTATTATTATTCACACAGCACACTTCTTAGGAGCTGGAGCTGGGCTACTAA	706
Qy	983	GTGCGTATGTTTATCAAGAGCTATACT	1009
Db	707	GTGCTTATATTATAAGAGCTATATT	733

RESULT 12	
CO094724	
LOCUS	827 bp mRNA linear EST 16-JUN-2004
DEFINITION	GR_Ea17A01.r GR__Ea Gossypium raimondii cDNA clone GR__Ea17A01.3,
	mRNA sequence.
ACCESSION	CO094724
VERSION	CO094724.1 GI:48793410
KEYWORDS	EST.
SOURCE	Gossypium raimondii
ORGANISM	Gossypium raimondii
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
	rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
REFERENCE	1. (bases 1 to 827)
AUTHORS	Kim, H., Yu, Y., Kudrna, D., Hafield, J., Stum, D., Mueller, C., Udall, J. A., Rapp, R. A., Wendel, J. F., Rao, K., Soderlund, C. and Wing, R. A.

ORIGIN	Query Match Best Local Similarity Matches 556; Conservative	19.1%; Score 416.2; DB 7; Length 827; 70.5%; Pred. No. 4.7e-88; 0; Mismatches 233; Indels 0; Gaps 0;	Wendle lab. Directional cloned into NotI-EV. Colonies plated/picked by AGI. More glycerol clones held in -80."
Qy	973	GGTCTGTAAGTGCGTATGTTATCAAGAAGCTATACTTTGGAAAGGCACCTCAACTGACCGA	1032
Db	37	GGGTGGTGTAGTCTTACATCATCAAAAAGTTCTACTTTGGAAAGGCACCTCAACAGATCGT	96
Qy	1033	GAGGTGCCCTTATGATGCTTATGGCGTATCTTTCTTATATGCTTGTGCTGAGCTTTTCGAC	1092
Db	97	GAATTTGCTCTTATGATGCTTATGGCATACCTTTTCGTATATCATATGCTGAACTGTTCTAT	156
Qy	1093	TTGAGCGGTATCCTCACTGTGTTTCTTCTGGGTATTTGTGATGTCCTCATATACACATGGCAC	1152
Db	157	TTGAGTGGCATCTTCACAGTATTTCTTTTGTGGGATTTGTGATGTCACATTATACCTGGCAC	216
Qy	1153	AATGTAAACGGAGAGCTCAAGATAAACAACAAAGCATACCTTTTGCACATTTTGTCAATTTCTT	1212
Db	217	AATGTTACAGAGAGTTCAAGAGTTACTACAAAGCATGCCCTTCTGCTACCTTGTCATTTGTT	276
Qy	1213	CGGAGACATTTATTTTCTTGTTATGTTGGAAATGGATGCCCTTGGACATTTGACAAGTGGAGA	1272
Db	277	GCTGAGACTTTTCTCTTTCTTTATATGTCGGGATGGATGCTTTTGGACATGGAGAAGTGGAGA	336
Qy	1273	TCCGTGAGTCACACACCGGGAACATCGATCGCAGTCAGCTCAATCTCAATGGCTCTGGTTC	1332
Db	337	TTTGTCAGTGATAGCCCTTGAAACGTAGTTGCTGTGTAGTGTCTGTCTGATGGGCTCTTGT	396
Qy	1333	ATGTTTGGAAAGACAGCGTTTCGTCTTTTCCGTTATCGTTTCTATCTAACTTAGGCCAAGAAG	1392
Db	397	ATGTTTGGAAAGACAGCTTTTGTGTTTCCCTGCTCATTTTATCCAACTTGGCCAAAGAAA	456
Qy	1393	AATCAAAAGCGAGAAAATCAACTTTAAATGATGAGTGTGATTTGGTGGTCTGTGCTCATG	1452
Db	457	TCAGCTAGTGAATAAATCAGCTTCAGGGAAACAAATTAATAATATGGTGGGCTGGGCTCATG	516
Qy	1453	AGAGGTGCTGATCTATGCTCTTTGGCTATGATCAACAAGTTTACAGGGCCGGGCACACAGAT	1512
Db	517	AGAGGCGCTGTATCTATGGCAGTTGATATAATATCAGTTTACAGGGGGGGGCCATCTCAG	576
Qy	1513	GTACGCGGGGAATGCAATCATGATCAGAGTACGATAAATCTGTCTGTCTTTTATAGCACAGTG	1572
Db	577	TTGCGAGGAATGCAATTTATGATTACAAGCAGTATAAACCATGTTCTTCTATTCAGCAGTGTG	636
Qy	1573	GTGTTTGGTATGCTGACAAACCACTCATAGCTACTATTACCGCACCAAGAGCGCAC	1632
Db	637	GTTTTTGGTTTAAATGACTAAACCTCTAAATAAGGTTCTTGTGTGCACATCCCAACCAACA	696
Qy	1633	ACGAGCATGTTATCTGATGACACACCCAAAATCCATACATATCCCTTTGTTGGACCAA	1692
Db	697	GCCAGCATGCTCTCAGACCAATCTACTCCAAAATCAATGGAGGCACTATTTCTCGGAAGC	756
Qy	1693	GACTCGTTCATGAGCCTTCAGGGAAACCAAAATGTGCTCGGCGCTGACAGTATACGTCGC	1752
Db	757	GGCCAGAGTCTTTTGTATGATAGTTTAAATGGAGTTTCATCGACCAACACGATTCGTGCA	816
Qy	1753	TTCTTGACA	1761
Db	817	CTTCTTACA	825

RESULT	l3
LOCUS	BE420587
DEFINITION	HW000.D12 ITEC HM Barley Leaf Library Hordeum vulgare subsp. vulgare cDNA clone HW000.D12, mRNA sequence.
ACCESSION	BE420587
VERSION	BE420587.1 GI:9418430
KEYWORDS	EST.
	linear EST 24-JUL-2000 1212 bp mRNA

SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
ORIGIN
Query Match
Best Local Similarity
Matches 614; Conservative 0; Mismatches 267; Indels 8; Gaps 3;
QY 587 AGCAGTTTTCGCAATTTTCGACTATTATGCTTTTGGTCTGTGGACTATTATTT 646
Db 61 AACAAATCTTCGCAATTTTCGACTATTATGCTTTTGGTCTGTGGACTATTATTT 120
QY 647 CTTCGCAATCATATCTCTAGGTGTAACAGATCTTTTAAAGATTGGACATGGAACCT 706
Db 121 CCTTCAGTATAATATACATGTTGGTCCATGGGCTAGTATCAAGGCTGAACATAGGCGCC 180
QY 707 TTGACTTGGGTGATTATCTTGTATTGGTGCCATATTTGCTGCAACAGATTTCAGTATGTA 766
Db 181 TTGAGCTTGGAGNACTACCTCGACTTGGGCAATATTTCTGGCAACGACTCTCTCGCA 240
QY 767 CACTGCAAGTTCTGAATCAAGACGACACCTTTGCTTTACAGTCTTGTATTTCGAGAGG 826
Db 241 CCTTGCAAGTTTAAAGCAAGATGACACACCTTTCTTGACAGTTTGGTGGTGGTGAAG 300
QY 827 GTGTTGTGAATGATGCAAGTCTAGTTGTGCTCTTCAACCGATTTCAGCTTTGATCTCA 886
Db 301 GTGTTGTGAATGATGCAAGTCTAGTTGTGCTCTTCAACCGATTTCAGCTTTGATCTTG 360
QY 887 CTCACCTAAACCAAGAGCTGCTTTTCATCTTCTGGAACCTCTTGTATTGTTTCTCC 946
Db 361 GAAATTTAGTAGGCTCAAAATCTTCAATTCATTCGAAATTCCTCTATCTATTGTTGGG 420
QY 947 TAAGTACCTTGTGTTGCTGCAACCGGCTGATAGTGGCTGATGTTATCAAGAACTAT 1006
Db 421 CCAGTACCTTTCTTGGAGTATCTAGTGACTTCTCAGTCTTATGTCATCAAGAACTGT 480
QY 1007 ACTTTGGAAGGCACTCAACTGACCGAGAGGTTGCCCTTATGATGCTTATGCGGTATCTTT 1066
Db 481 ACTTTGGCAGGCACTCCACTGATCGTGAAGTTGCTATTATGATGCTCATGGCTTATTAT 540

Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
1 (bases 1 to 1212)
Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T.,
Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A.,
Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J.,
Joudrier, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P.,
Ogihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G.,
Shariflou, M., Sorrells, M., Warburton, M., and Wenzel, G.
International Triticeae EST Cooperative (ITEC): Production of
Expressed Sequence Tags for Species of the Triticeae
Unpublished (2000)
Contact: Herrmann RG
Botanisches Institut der LMU
Menzinger Str. 67, D-80638 Munchen GERMANY
Fax: 49 30 171683
Email: herrmann@botanik.biologie.uni-muenchen.de
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
1..1212
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="barke"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="HWM000.D12"
/tissue_type="leaf"
/dev_stage="14 day old"
/clone_lib="ITEC HWM Barley Leaf Library"
/note="Vector: pBluescriptSK(-); 850 bp average insert
size."

RESULT 14
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
ORIGIN
Query Match
Best Local Similarity
Matches 614; Conservative 0; Mismatches 267; Indels 8; Gaps 3;
QY 587 AGCAGTTTTCGCAATTTTCGACTATTATGCTTTTGGTCTGTGGACTATTATTT 646
Db 61 AACAAATCTTCGCAATTTTCGACTATTATGCTTTTGGTCTGTGGACTATTATTT 120
QY 647 CTTCGCAATCATATCTCTAGGTGTAACAGATCTTTTAAAGATTGGACATGGAACCT 706
Db 121 CCTTCAGTATAATATACATGTTGGTCCATGGGCTAGTATCAAGGCTGAACATAGGCGCC 180
QY 707 TTGACTTGGGTGATTATCTTGTATTGGTGCCATATTTGCTGCAACAGATTTCAGTATGTA 766
Db 181 TTGAGCTTGGAGNACTACCTCGACTTGGGCAATATTTCTGGCAACGACTCTCTCGCA 240
QY 767 CACTGCAAGTTCTGAATCAAGACGACACCTTTGCTTTACAGTCTTGTATTTCGAGAGG 826
Db 241 CCTTGCAAGTTTAAAGCAAGATGACACACCTTTCTTGACAGTTTGGTGGTGGTGAAG 300
QY 827 GTGTTGTGAATGATGCAAGTCTAGTTGTGCTCTTCAACCGATTTCAGCTTTGATCTCA 886
Db 301 GTGTTGTGAATGATGCAAGTCTAGTTGTGCTCTTCAACCGATTTCAGCTTTGATCTTG 360
QY 887 CTCACCTAAACCAAGAGCTGCTTTTCATCTTCTGGAACCTCTTGTATTGTTTCTCC 946
Db 361 GAAATTTAGTAGGCTCAAAATCTTCAATTCATTCGAAATTCCTCTATCTATTGTTGGG 420
QY 947 TAAGTACCTTGTGTTGCTGCAACCGGCTGATAGTGGCTGATGTTATCAAGAACTAT 1006
Db 421 CCAGTACCTTTCTTGGAGTATCTAGTGACTTCTCAGTCTTATGTCATCAAGAACTGT 480
QY 1007 ACTTTGGAAGGCACTCAACTGACCGAGAGGTTGCCCTTATGATGCTTATGCGGTATCTTT 1066
Db 481 ACTTTGGCAGGCACTCCACTGATCGTGAAGTTGCTATTATGATGCTCATGGCTTATTAT 540

1067 CTTATATGCTTGTCTGAGCTTTTCGACTTGGAGCGGTATCTCTACTGTGTTTCTGTGTA 1126
541 CTTATATGCTTGTCTGAGCTTTTCGACTTGGAGCGGTATCTCTACTGTGTTTCTGTGTA 600
1127 TTGATGCTTGTCTGAGCTTTTCGACTTGGAGCGGTATCTCTACTGTGTTTCTGTGTA 1186
601 TTGATGCTTGTCTGAGCTTTTCGACTTGGAGCGGTATCTCTACTGTGTTTCTGTGTA 660
1187 ATACCTTGTGCAATTTTCGACTTGGAGCGGTATCTCTACTGTGTTTCTGTGTA 1246
661 ATGCTTGTGCAATTTTCGACTTGGAGCGGTATCTCTACTGTGTTTCTGTGTA 720
1247 ATGCTTGTGCAATTTTCGACTTGGAGCGGTATCTCTACTGTGTTTCTGTGTA 1301
721 ATGCTTGTGCAATTTTCGACTTGGAGCGGTATCTCTACTGTGTTTCTGTGTA 780
1302 CCGAGTGTGCAATTTTCGACTTGGAGCGGTATCTCTACTGTGTTTCTGTGTA 1361
781 TGCCTTGTGCAATTTTCGACTTGGAGCGGTATCTCTACTGTGTTTCTGTGTA 840
1362 GTTATGCTTGTGCAATTTTCGACTTGGAGCGGTATCTCTACTGTGTTTCTGTGTA 1421
841 TCTATGCTTGTGCAATTTTCGACTTGGAGCGGTATCTCTACTGTGTTTCTGTGTA 898
1422 GCAGTGTGCAATTTTCGACTTGGAGCGGTATCTCTACTGTGTTTCTGTGTA 1470
899 GCAAGTGTGCAATTTTCGACTTGGAGCGGTATCTCTACTGTGTTTCTGTGTA 946

CO085721 827 bp mRNA linear EST 16-JUN-2004
GR_Ea03A21.f GR_Ea Gossypium raimondii cDNA clone GR_Ea03A21 5',
mRNA sequence.
CO085721 GI:48776355
CO085721
EST.
Gossypium raimondii
Gossypium raimondii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases 1 to 827)
Kim, H., Yu, Y., Kudrna, D., Hatfield, J., Stum, D., Mueller, C.,
Udall, J.A., Rapp, R.A., Wendel, J.F., Rao, K., Soderlund, C. and
Wing, R.A.
Global assembly of Cotton ESTs
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
Plate: 03 row: A column: 21.
Location/Qualifiers
1..827
/organism="Gossypium raimondii"
/mol_type="mRNA"
/db_xref="taxon:29730"
/clone="GR_Ea03A21"
/tissue_type="whole seedlings"
/dev_stage="first true leaves"
/lab_host="DH10B"
/clone_lib="GR_Ea"
/note="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2:
EcoRV; Library made by Invitrogen with RNA supplied by
Wendle lab. Directional cloned into NotI-EV. Colonies
plated/picked by AGI. More glycerol clones held in -80."

Query Match 19.1%; Score 415; DB 7; Length 827;

between rice and Magnaporthe grisea Unpublished (2003) Contact: Rod Wing Arizona Genomics Institute University of Arizona Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ 85721-0088, USA Tel: 520 626 3967 Fax: 520 621 9288 Email: http://genome.arizona.edu		PCR Primers FORWARD: gta aaa cga cgg cca gtc g BACKWARD: gga aac agc tat gac cat g Plate: 08 row: D column: 05 Seq primer: gta aaa cga cgg cca gtc g.		Location/Qualifiers 1. -852 /organism="Oryza sativa (japonica cultivar-group)" /mol_type="mRNA" /cultivar="Nipponbare" /db_xref="taxon:39947" /clone="OSJNEf08D05" /tissue_type="Leaf" /dev_stage="3 week" /lab_host="DH10B" /notes="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2: XhoI; Uninfected Control"		Query Match 19.0%; Score 414.2; DB 6; Length 852; Best Local Similarity 67.9%; Pred. No. 1.4e-87; Matches 578; Conservative 0; Mismatches 273; Indels 0; Gaps 0;		QY 685 AAGAAGTTGACATTTGGAACCTTTGACTTGGGTGGATATCTTCTATTTGGTGCATATTT 744 Db 2 AAAAAAATTGATTTGGTCCACTCCAGCTTGGGGACTATCTTGCATTTGGGGTATCTTC 61 QY 745 GCTGCAACGATTCAGTATGTATGACTGCAGTGTCTGAATCAACAGACGAGACACCTTTGCTT 804 Db 62 TCAGCAACAGATTTCTTTTGGCACCTTACAGGTGCTTTAACAGACGAAACACCCCTACTC 121 QY 805 TACAGTCTTGATATTCGAGAGGGTGTGTGAATGATGCAACCGTCAGTGTGGTCTTCAAC 864 Db 122 TATAGTCTGGTTTTTGGTGAAGGGTGTCAATGATGCTACATCTGTGTGCTCTTTAAT 181 QY 865 GCGATTCAGAGCTTTGATCTCACTCACTTAACACGAGAGTCTTTTCACTCTCTTGG 924 Db 182 GCAATTGGAACATTTGATATTTGCTAAATTTGATAGCTTTGTTCTACTAGCGTTTCATAGGA 241 QY 925 AACTCTCTGATTTGTTTTCTCCTAAGTACCTTGTGTGGTGTGCTCAACCGCTCTGATAAGT 984 Db 242 AATTTCTCTACCTATCTTCCACAGTACCCTTCTTGGAGTAGTGTGCTGGTGTGCTTAGT 301 QY 985 GCGTATGTTATCAAGAAGCTATATCTTTTGGAAAGGCACTCAACTGACGAGAGGTGGCCCTT 1044 Db 302 GCCTATATATTAAAGAACTATGTTTTGGCAGACACTCAACTGACAGAGAAGTTGCTATC 361 QY 1045 ATGATGCTTATGCGGTATCTTTCTTATATGCTTGTGTGAGTGTTCGACTTTGACGGGTATC 1104 Db 362 ATGATACTCATGCGGTACCTTTTCATATATGCTGTCTAGATCTCTGAGTGGCAATT 431 QY 1105 CTCACCTGTGTTTTCTGTGTTATTTGATGTCCTCCATTACACATGGCACATGTAACGGAG 1164 Db 422 CTCACCTGTGTTCTCTCTGGAATAGTAATGTACATTACACTTTGGCATTAATGACAGAA 481 QY 1165 AGCTCAAGAATAACAACAAGCACTACTTTTGGAACTTTTGTCAACTTTTGTCAATTTCTTGGGAGACATTT 1224 Db 482 AGCTCTAGGATTACTACCAAGCACACTTTTGTCTCTTTATCTTTTCATTTGCTGAATTTT 541 QY 1225 ATTTCTTGTATGTTTGGAAATGGAGTCTTGGACATTTGACAAATGACAAAGTGGAGATCCGCTGAGTGAC 1284 Db 542 CTATTTCTCTATCTTGGGATGGATGACATGCAATGAAAAATGAAAAATGAAAAATGATGATGACG 601	
JOURNAL COMMENT		FEATURES		ORIGIN					
Contact: Rod Wing		PCR Primers		/notes="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2: XhoI; Uninfected Control"		Query Match 19.0%; Score 414.2; DB 6; Length 852; Best Local Similarity 67.9%; Pred. No. 1.4e-87; Matches 578; Conservative 0; Mismatches 273; Indels 0; Gaps 0;		QY 685 AAGAAGTTGACATTTGGAACCTTTGACTTGGGTGGATATCTTCTATTTGGTGCATATTT 744 Db 2 AAAAAAATTGATTTGGTCCACTCCAGCTTGGGGACTATCTTGCATTTGGGGTATCTTC 61 QY 745 GCTGCAACGATTCAGTATGTATGACTGCAGTGTCTGAATCAACAGACGAGACACCTTTGCTT 804 Db 62 TCAGCAACAGATTTCTTTTGGCACCTTACAGGTGCTTTAACAGACGAAACACCCCTACTC 121 QY 805 TACAGTCTTGATATTCGAGAGGGTGTGTGAATGATGCAACCGTCAGTGTGGTCTTCAAC 864 Db 122 TATAGTCTGGTTTTTGGTGAAGGGTGTCAATGATGCTACATCTGTGTGCTCTTTAAT 181 QY 865 GCGATTCAGAGCTTTGATCTCACTCACTTAACACGAGAGTCTTTTCACTCTCTTGG 924 Db 182 GCAATTGGAACATTTGATATTTGCTAAATTTGATAGCTTTGTTCTACTAGCGTTTCATAGGA 241 QY 925 AACTCTCTGATTTGTTTTCTCCTAAGTACCTTGTGTGGTGTGCTCAACCGCTCTGATAAGT 984 Db 242 AATTTCTCTACCTATCTTCCACAGTACCCTTCTTGGAGTAGTGTGCTGGTGTGCTTAGT 301 QY 985 GCGTATGTTATCAAGAAGCTATATCTTTTGGAAAGGCACTCAACTGACGAGAGGTGGCCCTT 1044 Db 302 GCCTATATATTAAAGAACTATGTTTTGGCAGACACTCAACTGACAGAGAAGTTGCTATC 361 QY 1045 ATGATGCTTATGCGGTATCTTTCTTATATGCTTGTGTGAGTGTTCGACTTTGACGGGTATC 1104 Db 362 ATGATACTCATGCGGTACCTTTTCATATATGCTGTCTAGATCTCTGAGTGGCAATT 431 QY 1105 CTCACCTGTGTTTTCTGTGTTATTTGATGTCCTCCATTACACATGGCACATGTAACGGAG 1164 Db 422 CTCACCTGTGTTCTCTCTGGAATAGTAATGTACATTACACTTTGGCATTAATGACAGAA 481 QY 1165 AGCTCAAGAATAACAACAAGCACTACTTTTGGAACTTTTGTCAACTTTTGTCAATTTCTTGGGAGACATTT 1224 Db 482 AGCTCTAGGATTACTACCAAGCACACTTTTGTCTCTTTATCTTTTCATTTGCTGAATTTT 541 QY 1225 ATTTCTTGTATGTTTGGAAATGGAGTCTTGGACATTTGACAAATGACAAAGTGGAGATCCGCTGAGTGAC 1284 Db 542 CTATTTCTCTATCTTGGGATGGATGACATGCAATGAAAAATGAAAAATGAAAAATGATGATGACG 601	

between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aaa cgg cca gtc g
BACKWARD: gga aac agc tat gac cat g
Plate: 08 row: D column: 05
Seq primer: gta aaa cga cgg cca gtc g.
Location/Qualifiers
1..852
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSUNEF08D05"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEF"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; Uninfected Control"

ORIGIN									
Query Match 19.0%; Score 414.2; DB 6; Length 852; Best Local Similarity 67.9%; Pred. No. 1.4e-87; Matches 578; Conservative 0; Mismatches 273; Indels 0; Gaps 0;									
QY	685	AAGAAGTTGGACATTTGAAACCTTTGACTTGGGTGATTTATCTTTGTTGGCGCATATTT	744						
Db	2	AAAAAATCTGATTTGGTCCACTCCAGCTTGGGACTATCTTGCAATTTGGGGCTATCTTC	61						
QY	745	GCTGCACAGATTCAGTATGTACACTGCAGTTTCTGAATCAAGACGAGACACCTTTGCTT	804						
Db	62	TCAGCAACAGATTCGTTTGCACCTTACAGTGTCTTAACCAAGACGAAACCCCTACTC	121						
QY	805	TACAGTCTTGATTCGGAGAGGGTGTGTGAATCATGCAACGTCAGTTTGGTCTTCAAC	864						
Db	122	TATAGTCTGTTTGGTGAAGGGTGTCAATCATGCTACATCTGTTGTCTCTTAAAT	181						
QY	865	GCGATTGAGCTTTGATCTCCTACCTAAACCAACGAAAGCTGCTTTTCATCTCTTGGGA	924						
Db	182	GCAATTCGAAGACATGATATTTGCTAAATTTTGATAGCCTTGTCTACTAGCGTTCATAGGA	241						
QY	925	AACCTCTTGATTTGTTCTTCCCTAAGTACCTTGTGTTGGTGTCTGCAACCGGCTCATAGT	984						
Db	242	AATTTCTCTACCTATTCTTCCACGAGTACCCCTTCTTGGAGTAGTGTGCTGGGTGCTTAGT	301						
QY	985	GCGTATGTTATCAAGAAGCTATCTTTGGAAGGCACTCAACTGACCGAGAGTTGCCCTT	1044						
Db	302	GCCTATATTAAGAAGCACTATGTTTGGCAGACATCTCACTGACAGAGTTGCTATC	361						
QY	1045	ATGATGCTTATGGCGTATCTTTCTTATATGCTTGTGAGCTTTTCGACTTGAGCGGTATC	1104						
Db	362	ATGATGCTATGCGGTACCTTTTCATATATGCTGCTGATGCTGTAGATCTGAGTGGCAT	421						
QY	1105	CTCACTGTTTTTCTGTGGTATTGTGATGTCCCATTTACATCATGCGCAATGTAAACGAG	1164						
Db	422	CTCACTGTGTTCTTCTCTGGAATAGTAATGTACATTTACACTTGGCATTAATGTGACAGAA	481						
QY	1165	AGCTCAAGAAATAACAACAAGCATACCTTTTGCAACTTTGTCAATTTCTTGGCGAGACATTT	1224						
Db	482	AGCTCTAGGATTAATACAGCACACTTTTGTCTACTTTTCACTTTCTGCTGAAATTTT	541						
QY	1225	ATTTTCTTGTATGTTGGAATGAGTCCCTTGGACATTTGACAAAGTGGAGATCCGTGAGTGAC	1284						
Db	542	CTATTTCTTATGTTGGATGGAATGCACTGGACATTTGAAAAATGAAAAATAGCTAGCAGC	601						

Qy	1285	ACACCGGGAACATCGATCGCAGTGAGCTCAATCCTAATGGGCTCTGGTCAATGGTTGGAAGA	1344
Db	602	AGTCTAAAACCAATTTGCTTTTAAGTGCACACTATATGGGCTTGGTTATGGTTGGAAGA	661
Qy	1345	GCACGGTTCGTCCTTTCCGGTTATCGTTTCTATCTAACTTAGCCAAAGAAGAAATCAACGCGAG	1404
Db	662	GCAGCATTTGTAATCCCTTTTGTCTTTCTTATCCAACTAAGTAAAAAGNAGACACGCCCA	721
Qy	1405	AAAATCAACTTTAAATCATGCAGGTTTGATTTGGTGTCTGGTCTCATATGAGAGGTGCTGTA	1464
Db	722	AAGATCTCCTTCAAGCAGCAAGTAATCATATGTTGGGCGAGGTCTCATATGAGAGGAGCAGTA	781
Qy	1465	TCATATGCTCTTTGCATACAAACAAGTTTACAAGGGCCGGGCACACAGATGTACGCGGGAAT	1524
Db	782	TCAATAGCACTTGCCTATCACAAGTTTCACCGCATCTGGTCTATACTGAATTCGGAATCAT	841
Qy	1525	GCAATCATGAT	1535
Db	842	GCTATCATGAT	852

Search completed: August 28, 2005, 07:36:19
Job time : 7209 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 27, 2005, 22:06:40 ; Search time 1181 Seconds
(without alignments)
10917.186 Million cell updates/sec

Title: US-10-617-624-1

Perfect score: 2178

Sequence: 1 cctctctgttctgtctctgcg.....aaaaaaaaaaaaaaaaaaaaa 2178

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: N_Geneseq_16Dec04:*
- 2: Geneseqn1980s:*
- 3: Geneseqn1990s:*
- 4: Geneseqn2000s:*
- 5: Geneseqn2001as:*
- 6: Geneseqn2001bs:*
- 7: Geneseqn2002as:*
- 8: Geneseqn2002bs:*
- 9: Geneseqn2003as:*
- 10: Geneseqn2003bs:*
- 11: Geneseqn2003cs:*
- 12: Geneseqn2003ds:*
- 13: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2178	100.0	2178	2	Aaz22591 Arabidops
2	2143.4	98.4	2284	2	Aaz22595 Arabidops
3	1617	74.2	1617	6	Abz13434 Arabidops
4	1617	74.2	1617	12	Adn74230 Thale cre
5	1614	74.1	1614	12	Adn11979 Wild type
6	1612.4	74.0	1614	12	Adn11981 AtHNX1 mu
7	1563	71.8	1563	12	Adn11983 AtHNX1 mu
8	1563	71.8	1566	12	Adn11989 AtHNX1 mu
9	1473	67.6	1473	12	Adn11985 AtHNX1 mu
10	1407	64.6	1410	12	Adn11991 NDL-2 enc
11	1362	62.5	1362	12	Adn11987 AtHNX1 mu
12	1320.4	60.6	1323	12	Adn11993 NDL-3 enc
13	848	38.9	1449	12	Adm68265 Plant Na+
14	832.8	38.2	1568	3	Aaa72926 Atllipex
15	821.2	37.7	2553	4	Aaf75765 Gene regu
16	813	37.3	2423	4	Aaf75764 Gene regu
17	806.4	37.0	1668	6	Acc49921 Suaeda sa
18	806.4	37.0	2397	6	Acc49920 Suaeda sa
19	805.4	37.0	1315	12	Adm68266 Arabidops
20	797.6	36.6	1620	10	Adj99891 Potato sa

21	794.4	36.5	1621	10	ADJ99890	Adj99890 Potato sa
22	774.8	35.6	2237	4	AAF75752	Aaf75752 Gene regu
23	768.8	35.3	2330	3	AAa61876	Aaa61876 cDNA enc
24	754.4	34.6	2361	4	AAF75766	Aaf75766 Gene regu
25	682.6	31.3	1638	10	ACF58165	Acf58165 Z. mays s
26	651	29.9	1955	11	ADM82830	Adm82830 Agropyron
27	523.8	24.0	1788	2	AAZ22592	Aaz22592 Arabidops
28	491.6	22.6	1674	6	ABX12638	Abx12638 DNA encod
29	418	19.2	418	8	ABX62293	Abx62293 Arabidops
30	401.8	18.4	1740	12	ADM68263	Adm68263 Mangrove
31	269.2	12.4	612	13	ACN53419	Acn53419 Cotton an
32	252.6	11.6	330	2	AAZ22611	Aaz22611 Arabidops
33	226.4	10.4	378	2	AAZ22606	Aaz22606 Rice Na/H
34	191	8.8	613	10	ADD17688	Add17688 DNA (SeqI
35	165.2	7.6	466	12	ADP94869	Adp94869 Cotton ex
36	165.2	7.6	466	13	ADR62082	Adr62082 Cotton cd
37	153.2	7.0	588	10	ADD17689	Add17689 DNA (SeqI
38	152.2	7.0	573	13	ACN47580	Acn47580 Cotton pr
39	149.4	6.9	596	13	ACN60354	Acn60354 Cotton gy
40	146.4	6.7	2000	6	ABZ16128	Abz16128 Arabidops
41	141.8	6.5	1824	3	AAc95373	Aac95373 Cat flea
42	141.8	6.5	1824	3	AAc95372	Aac95372 Cat flea
43	141.8	6.5	2080	3	AAc95370	Aac95370 Cat flea
44	141.8	6.5	2080	3	AAc95371	Aac95371 Cat flea
45	125	5.7	281	6	ABL73323	Ab173323 Corn tass

ALIGNMENTS

RESULT 1
AAZ22591
ID AAZ22591 standard; cDNA; 2178 BP.

AC AAZ22591;

DT 18-JAN-2000 (first entry)

DE Arabidopsis thaliana Na/H transporter gene AtNHX1.

KW Sodium; proton; antiport; transporter; salt tolerance; salt management;
transgenic plant; survival; soil; farming; accumulation; irrigation;
crop; ss.

OS Arabidopsis thaliana.

PN WO9947679-A2.

PD 23-SEP-1999.

PF 18-MAR-1999; 99WO-CA000219.

PR 18-MAR-1998; 98US-0078474P.

PR 15-JAN-1999; 99US-0116111P.

(BLUM/) BLUMWALD E.

(APSE/) APSE M.

(SNED/) SNEDDEN W.

(AHAR/) AHARON G.

Blumwald E, Apse M, Snedden W, Aharon G;

WPI; 1999-571840/48.

P-FSDB; AAY40901.

Nucleic acid molecules encoding sodium/proton transport polypeptides,
useful in genetic engineering salt tolerance in crop plants.

Claim 4; Fig 1A; 93pp; English.

The invention relates to an isolated nucleic acid molecule encoding a
plant Na/H antiport (PNHX) transporter polypeptide, or a fragment and
capable of increasing salt tolerance in a cell. This sequence corresponds

CC to the gene encoding the AtNHX1 transporter from Arabidopsis thaliana.
CC The Na/H transporter polypeptides provide a means of intracellular salt
CC management, particularly in plants. the sequences are useful for
CC producing transgenic plants that are capable of surviving in soil with
CC high salt levels that would normally inhibit growth of the crop species.
CC This would be useful in farming land in areas that are generally
CC considered unproductive through salt accumulation and poor irrigation,
CC e.g. in India, Australia, and prairies in USA or Canada. Commercial
CC crops, such as potatoes, tomatoes, brassica, cotton, sunflower,
CC strawberries, spinach, lettuce, rice, soybean, corn, wheat, rye, barley,
CC atriplex, sorghum, alfalfa, salicornia and others would benefit from
CC increased salt tolerance
XX

SQ Sequence 2178 BP; 576 A; 413 C; 472 G; 717 T; 0 U; 0 Other;

Query Match 100.0%; Score 2178; DB 2; Length 2178;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCTCTGTTTCGTTCTGTTAGACGAGAGAGAGAAATCTCAGGTTTAGCTTTCGA 60
DB 1 CCTCTCTGTTTCGTTCTGTTAGACGAGAGAGAGAAATCTCAGGTTTAGCTTTCGA 60
QY 61 AGCTTCCAAAATTTTGAATTTTGATCTCTCGGCTCTTTTGTAAATCAGACTGAAGATAT 120
DB 61 AGCTTCCAAAATTTTGAATTTTGATCTCTCGGCTCTTTTGTAAATCAGACTGAAGATAT 120
QY 121 TTAAATACCCAGAAAGTTGTTCAAGAAATGTTTCAGTGGACAGACCGGAAGATAAAG 180
DB 121 TTAAATACCCAGAAAGTTGTTCAAGAAATGTTTCAGTGGACAGACCGGAAGATAAAG 180
QY 181 AGACTTTTTTTCAGATTTTGCTGATCCAAATCTGAATAGTTGTTTCTTGGAT 240
DB 181 AGACTTTTTTTCAGATTTTGCTGATCCAAATCTGAATAGTTGTTTCTTGGAT 240
QY 241 CAAATCTCGAAAGAGAAATTTGTTGGATCTAGAAGAGATAAACAATGTTGATCTCTA 300
DB 241 CAAATCTCGAAAGAGAAATTTGTTGGATCTAGAAGAGATAAACAATGTTGATCTCTA 300
QY 301 GTGTCGAAATGCTTTCGTTATCGACATCTGATCAGCTTCTGTGGTTGCGTTGAATCTC 360
DB 301 GTGTCGAAATGCTTTCGTTATCGACATCTGATCAGCTTCTGTGGTTGCGTTGAATCTC 360
QY 361 TTTGTTGACACTTCTTGTGCTGTTATGTTCTTGTGTCATCTTTTGGAAAGAAATAGATGG 420
DB 361 TTTGTTGACACTTCTTGTGCTGTTATGTTCTTGTGTCATCTTTTGGAAAGAAATAGATGG 420
QY 421 ATGAACGAATCCATCACCGCCTTGTGTTGATTTGGCTTAGGCATCTGTTTACCAATTTGTTG 480
DB 421 ATGAACGAATCCATCACCGCCTTGTGTTGATTTGGCTTAGGCATCTGTTTACCAATTTGTTG 480
QY 481 ATTAGTAAAGGAAAAAGCTCGCATCTTCTGCTTTTATGGAAGATCTTTTCTTCATATAT 540
DB 481 ATTAGTAAAGGAAAAAGCTCGCATCTTCTGCTTTTATGGAAGATCTTTTCTTCATATAT 540
QY 541 CTTTTCGCCACCATTTATATTCAATCGAGGTTTCAAGTAAAAAAGACGAGTTTTCGCG 600
DB 541 CTTTTCGCCACCATTTATATTCAATCGAGGTTTCAAGTAAAAAAGACGAGTTTTCGCG 600
QY 601 AATTTTCGTGACTATTATGCTTTTGGTCTGTTGGGACTATTATTCTTTCGACAAATCATAT 660
DB 601 AATTTTCGTGACTATTATGCTTTTGGTCTGTTGGGACTATTATTCTTTCGACAAATCATAT 660
QY 661 TCTCTAGGTGTAACACAGTTCTTTAAGAAAGTTGGACATTTGGAACCTTTGACTTGGGTGAT 720
DB 661 TCTCTAGGTGTAACACAGTTCTTTAAGAAAGTTGGACATTTGGAACCTTTGACTTGGGTGAT 720
QY 721 TATCTTGTATTTGGTGCCATATTTGCTGCAACAGATTGATGATGACTGCGAGTTCTG 780
DB 721 TATCTTGTATTTGGTGCCATATTTGCTGCAACAGATTGATGATGACTGCGAGTTCTG 780
QY 781 AATCAAGACGACACCTTTGCTTTTACAGTCTTGTATTTCGAGAGGGTGTGTGAATGAT 840
DB 781 AATCAAGACGACACCTTTGCTTTTACAGTCTTGTATTTCGAGAGGGTGTGTGAATGAT 840

DB 781 AATCAAGACGACACCTTTGCTTTTACAGTCTTGTATTTCGAGAGGGTGTGTGAATGAT 840
QY 841 GCAACGTCAGTTTGGTCTTCAACGCGAATTCAGAGCTTTGATCTCCTCCTCAACCTAACCCAC 900
DB 841 GCAACGTCAGTTTGGTCTTCAACGCGAATTCAGAGCTTTGATCTCCTCCTCAACCTAACCCAC 900
QY 901 GAAGCTGCTTTTCACTCTTCTTGGAAACTCTTGTGATTTGTTTCTTCCCTAAGTACCTTGCTT 960
DB 901 GAAGCTGCTTTTCACTCTTCTTGGAAACTCTTGTGATTTGTTTCTTCCCTAAGTACCTTGCTT 960
QY 961 GGTCTGCAACCGGTCTGATAAGTGCATGTTATCAAGAAGCTATATCTTTGGAAGGCAC 1020
DB 961 GGTCTGCAACCGGTCTGATAAGTGCATGTTATCAAGAAGCTATATCTTTGGAAGGCAC 1020
QY 1021 TCAACTGACGAGAGGTTGGCTTTATGATGCTTATGGCGTATCTTTCTTATATATCTTGCT 1080
DB 1021 TCAACTGACGAGAGGTTGGCTTTATGATGCTTATGGCGTATCTTTCTTATATATCTTGCT 1080
QY 1081 GAGCTTTTCGACTTGAAGGCTATCTCTCACTGTTGTTTTCTGTGCTATTTGTGATGTCCTCAT 1140
DB 1081 GAGCTTTTCGACTTGAAGGCTATCTCTCACTGTTGTTTTCTGTGCTATTTGTGATGTCCTCAT 1140
QY 1141 TACACATGGCAATGTAAACGAGAGCTCAAGAAATAACAACAAGCATACCTTTGCAACT 1200
DB 1141 TACACATGGCAATGTAAACGAGAGCTCAAGAAATAACAACAAGCATACCTTTGCAACT 1200
QY 1201 TTGTCATTTCTGCGGAGACATTTATTTCTTGTGATGTTGGAAATGGATGCTTGGACATTT 1260
DB 1201 TTGTCATTTCTGCGGAGACATTTATTTCTTGTGATGTTGGAAATGGATGCTTGGACATTT 1260
QY 1261 GACAAGTGGAGATCCGTTGAGTGACACACCGGAACTCGATCGCAGTGAGCTCAATCTTA 1320
DB 1261 GACAAGTGGAGATCCGTTGAGTGACACACCGGAACTCGATCGCAGTGAGCTCAATCTTA 1320
QY 1321 ATGGGTCGTGTCATGTTGGAAGACGAGCTTCTGCTTTCCGTTATCGTTTCTATCTAAC 1380
DB 1321 ATGGGTCGTGTCATGTTGGAAGACGAGCTTCTGCTTTCCGTTATCGTTTCTATCTAAC 1380
QY 1381 TTAGCCAAAGAAATCAAAACGAGAAATCAATCTTAAACATGCAAGTTGTTGATTTGGTGG 1440
DB 1381 TTAGCCAAAGAAATCAAAACGAGAAATCAATCTTAAACATGCAAGTTGTTGATTTGGTGG 1440
QY 1441 TCTGCTCTCATGAGAGTGTGTTATCTATGCTCTTGCATACAAAGTTTACAAAGGCGC 1500
DB 1441 TCTGCTCTCATGAGAGTGTGTTATCTATGCTCTTGCATACAAAGTTTACAAAGGCGC 1500
QY 1501 GGGCACACAGATGTACGCGGGAATGCAATCATGATCAAGTACGATACTGCTGCTT 1560
DB 1501 GGGCACACAGATGTACGCGGGAATGCAATCATGATCAAGTACGATACTGCTGCTT 1560
QY 1561 TTTAGCACAGTGTGTTGTTATGCTGACCAACCACTCATAGCTACCTTATTAACCGCAC 1620
DB 1561 TTTAGCACAGTGTGTTGTTATGCTGACCAACCACTCATAGCTACCTTATTAACCGCAC 1620
QY 1621 CAGAACCCACACGAGCATGTTATCTGATGACAAACCCCAAAATCCATACATATCCCT 1680
DB 1621 CAGAACCCACACGAGCATGTTATCTGATGACAAACCCCAAAATCCATACATATCCCT 1680
QY 1681 TTGTTGGACCAAGACTCGTTTCAATTTGAGCCTTCAGGAAACCAATGTCGCTCGCCTGAC 1740
DB 1681 TTGTTGGACCAAGACTCGTTTCAATTTGAGCCTTCAGGAAACCAATGTCGCTCGCCTGAC 1740
QY 1741 AGTATAGTGGCTTCTTGAACGCGCCCATCTCGAAACCGTGCAATTAATACTGAGACAATTT 1800
DB 1741 AGTATAGTGGCTTCTTGAACGCGCCCATCTCGAAACCGTGCAATTAATACTGAGACAATTT 1800
QY 1801 GATGACTCTTCTATGCGACCCGCTTTTGGAGGCTGCTGCTTTGTACCTTTGTTTCCAGGT 1860
DB 1801 GATGACTCTTCTATGCGACCCGCTTTTGGAGGCTGCTGCTTTGTACCTTTGTTTCCAGGT 1860
QY 1861 TCTCAACTGAGAGAAACCCCTCTCTGATCTTAGTAGGCTTGGAGGTAACGTTGGAAGAAA 1920
DB 1861 TCTCAACTGAGAGAAACCCCTCTCTGATCTTAGTAGGCTTGGAGGTAACGTTGGAAGAAA 1920

RESULT 2	
AAZ22595	
ID	AAZ22595 standard; cDNA; 2284 BP.
XX	
XX	AAZ22595;
XX	
DT	18-JAN-2000 (first entry)
XX	
XX	Arabidopsis thaliana Na/H transporter gene.
DE	
DE	Sodium; proton; antiport; transporter; salt tolerance; salt management;
KW	transgenic plant; survival; soil; farming; accumulation; irrigation;
KW	crop; ss.
XX	
XX	Arabidopsis thaliana.
OS	
XX	WO9947679-A2.
PN	
XX	23-SEP-1999.
PD	
XX	18-MAR-1999; 99WO-CA000219.
PF	
XX	18-MAR-1998; 98US-0078474P.
PR	
PR	15-JAN-1999; 99US-0116111P.
XX	
XX	(BLUM/) BLUMWALD E.
PA	(APSE/) APSB M.
PA	(SNED/) SNEEDEN W.
PA	(AHAR/) AHARON G.
XX	
PI	Blumwald E, Apse M, Snedden W, Aharon G;
XX	
DR	WPI; 1999-571840/48.
DR	P-PSDB; AAY40905.
XX	
PT	Nucleic acid molecules encoding sodium/proton transport polypeptides,
PT	useful in genetic engineering salt tolerance in crop plants.
XX	
PS	Claim 48; Fig 5A-B; 93pp; English.
XX	
CC	The invention relates to an isolated nucleic acid molecule encoding a
CC	plant Na/H antiport (PNHX) transporter polypeptide, or a fragment and
CC	capable of increasing salt tolerance in a cell. This sequence corresponds
CC	to the gene encoding a transporter from Arabidopsis thaliana. The Na/H
CC	transporter polypeptides provide a means of intracellular salt
CC	management, particularly in plants. The sequences are useful for
CC	producing transgenic plants that are capable of surviving in soil with
CC	high salt levels that would normally inhibit growth of the crop species.
CC	This would be useful in farming land in areas that are generally
CC	considered unproductive through salt accumulation and poor irrigation
CC	e.g. in India, Australia, and prairies in USA or Canada. Commercial

CC E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to
CC alter plant characteristics accordingly. The present invention describes
CC generating transgenic plants for the production of growth regulators,
CC enzymes, therapeutics, pharmaceuticals and animal feed products, where
CC the altered plant characteristics are selected from increased yield or
CC biomass, enhanced survival capacity, stress tolerance, plant architecture
CC or physiology, altered endoreduplication, biochemistry, signal
CC transduction, storage lipid mobilisation and/or altered photosynthesis,
CC each relative to the corresponding wild type plants. Accordingly, these
CC sequences can also be useful as positive or negative selectable markers
CC during transformation of cells or tissues. The identified genes play a
CC role in a variety of biological processes such as DNA replication, cell
CC wall biosynthesis, nitrogen and/ or carbon metabolism or they function as
CC transcription factors. This polynucleotide sequence is thale cress cDNA
CC repressed 1.3 fold or more in plants overexpressing the E2Fa/Dpa
CC transcription factor, given in an exemplification of the invention.
XX
SQ Sequence 1617 BP; 389 A; 346 C; 359 G; 523 T; 0 U; 0 Other;

Query Match 74.2%; Score 1617; DB 12; Length 1617;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1617; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 286 ATGTGGATCTCTAGTGTGAAACTGCTTCGTTATCGACATCTGATCAAGCTTCGTG 345
DB 1 ATGTGGATCTCTAGTGTGAAACTGCTTCGTTATCGACATCTGATCAAGCTTCGTG 60

QY 346 GTTGGTGAATCTCTTTGTGCACTCTTTGTGCTTGTATGTTTGTGGTCACTTTTG 405
DB 61 GTTGGTGAATCTCTTTGTGCACTCTTTGTGCTTGTATGTTTGTGGTCACTTTTG 120

QY 406 GAAGAGATAGATGATCAACGATCCATCCATCACCGCTTGTGATTTGGCTAGGCACGTGT 465
DB 121 GAAGAGATAGATGATGAAAGATCCATCACCGCTTGTGATTTGGCTAGGCACGTGT 180

QY 466 GTTACATTTTGTGATTAAGAAAGAAAGCTCGCATCTTCTCGTCTTTAGTGAAGAT 525
DB 181 GTTACATTTTGTGATTAAGAAAGAAAGCTCGCATCTTCTCGTCTTTAGTGAAGAT 240

QY 526 CTTTCTTCATATATCTTTTGGCCACCCATATATTAATCAATGAGGTTTCAAGTAAAG 585
DB 241 CTTTCTTCATATATCTTTTGGCCACCCATATATTAATCAATGAGGTTTCAAGTAAAG 300

QY 586 AAGCAGTTTTCGCAATCTCGTACTATATGCTTTTGTGCTTGTGGTGGTCACTATATT 645
DB 301 AAGCAGTTTTCGCAATCTCGTACTATATGCTTTTGTGCTTGTGGTGGTCACTATATT 360

QY 646 TCTTGCAATATATCTCTAGGTGTAACAGATTTCTTTAAGAGAGTTGGACATTTGAACC 705
DB 361 TCTTGCAATATATCTCTAGGTGTAACAGATTTCTTTAAGAGAGTTGGACATTTGAACC 420

QY 706 TTTGACTGGGTGATATCTTGCTATTTGGTGCATATTTTGTGCAACAGATTCAGTATGT 765
DB 421 TTTGACTGGGTGATATCTTGCTATTTGGTGCATATTTTGTGCAACAGATTCAGTATGT 480

QY 766 ACATGCAAGTTCTGAATCAAGACAGACCTTTGCTTACGTTCTGTATTCGGAGAG 825
DB 481 ACATGCAAGTTCTGAATCAAGACAGACCTTTGCTTACGTTCTGTATTCGGAGAG 540

QY 826 GGTGTGTGAATGATGCAACGTCAGTTGTGTCTTCAACGGGATTCAGAGCTTTGATCTC 885
DB 541 GGTGTGTGAATGATGCAACGTCAGTTGTGTCTTCAACGGGATTCAGAGCTTTGATCTC 600

QY 886 ACTACCTAAACCAAGAGCTGCTTTTCATCTTCTTTGGAACCTTCTTGTATTTGTTTCTC 945
DB 601 ACTACCTAAACCAAGAGCTGCTTTTCATCTTCTTTGGAACCTTCTTGTATTTGTTTCTC 660

QY 946 CTAAGTACTTGTGCTGCTGCAACCGTCTGATAAGTGGTATGTTATCAAGAGCTA 1005
DB 661 CTAAGTACTTGTGCTGCTGCAACCGTCTGATAAGTGGTATGTTATCAAGAGCTA 720

QY 1006 TACTTTGGAAGGCACTCAACTGACCGAGAGGTTGCGCTTATGATCTTATGGCGTATCTT 1065
|||||

DB 721 TACTTTGGAAGGCACTCAACTGACCGAGAGGTTGCCCTTATGATGCTTATGGCGTATCTT 780
QY 1066 TCTTATATGCTTGTGCTAGCTTTTCGACTTGAGCGGTATCCTCACTGTGTTTTCCTGGT 1125
DB 781 TCTTATATGCTTGTGCTAGCTTTTCGACTTGAGCGGTATCCTCACTGTGTTTTCCTGGT 840
QY 1126 ATTGTGATGTCCTCATTTACATGSCACAATGTAAAGGAGAGTCTCAAGATTAACAACAAG 1185
DB 841 ATTGTGATGTCCTCATTTACATGSCACAATGTAAAGGAGAGTCTCAAGATTAACAACAAG 900
QY 1186 CATACCTTTGCAACTTTTGTGCTTTCTTGGAGACATTTATTTTCTGTATGTTGGATG 1245
DB 901 CATACCTTTGCAACTTTTGTGCTTTCTTGGAGACATTTATTTTCTGTATGTTGGATG 960
QY 1246 GATGCTTTGGACATTTGACATGAGATCCGTGATGTCACACACCGGGAACATTCGATCGCA 1305
DB 961 GATGCTTTGGACATTTGACATGAGATCCGTGATGTCACACACCGGGAACATTCGATCGCA 1020
QY 1306 GTGAGCTCAATCCTTAATGGGTCTGCTCATGTTTGAAGAGCAGCGTTCTGTTCCGTTA 1365
DB 1021 GTGAGCTCAATCCTTAATGGGTCTGCTCATGTTTGAAGAGCAGCGTTCTGTTCCGTTA 1080
QY 1366 TCGTTTCTATCTAATCTTAGCCAAAGAAATCAAAAGCGAGAAATCAAATTTAAACATGAG 1425
DB 1081 TCGTTTCTATCTAATCTTAGCCAAAGAAATCAAAAGCGAGAAATCAAATTTAAACATGAG 1140
QY 1426 GTTGTGATTTGGTGTCTGCTCATGAGAGGTGCTGTATCTATGCTTCTTGGATACAAAC 1485
DB 1141 GTTGTGATTTGGTGTCTGCTCATGAGAGGTGCTGTATCTATGCTTCTTGGATACAAAC 1200
QY 1486 AAGTTTAAAGGGCGGGCACACAGATGTACGGGGAAATGCAATCATGATCACCAGTACG 1545
DB 1201 AAGTTTAAAGGGCGGGCACACAGATGTACGGGGAAATGCAATCATGATCACCAGTACG 1260
QY 1546 ATAACTCTCTGCTCTTTTGTAGCACAGTGTGTTTGGTATGCTGACCAACCACTCATAGC 1605
DB 1261 ATAACTCTCTGCTCTTTTGTAGCACAGTGTGTTTGGTATGCTGACCAACCACTCATAGC 1320
QY 1606 TACCTATTACGGCACCAAGAGCCACACAGAGCATGTTTCTGATGACACACACCCCAAAA 1665
DB 1321 TACCTATTACGGCACCAAGAGCCACACAGAGCATGTTTCTGATGACACACACCCCAAAA 1380
QY 1666 TCCATACATATCCCTTTTGGACCAAGACTCGTTTCAATGAGCCTTCAGGGAAACCAAT 1725
DB 1381 TCCATACATATCCCTTTTGGACCAAGACTCGTTTCAATGAGCCTTCAGGGAAACCAAT 1440
QY 1726 GTGCTTCGGCTGACAGTATACGTGGCTTCTTGAACGGCCCACTCGAACCGTGCATPAC 1785
DB 1441 GTGCTTCGGCTGACAGTATACGTGGCTTCTTGAACGGCCCACTCGAACCGTGCATPAC 1500
QY 1786 TACTGGAGACATTTGATGACTCCTTTCATGGAGCCCTCTTTGGAGGTCTGGCTTTGTA 1845
DB 1501 TACTGGAGACATTTGATGACTCCTTTCATGGAGCCCTCTTTGGAGGTCTGGCTTTGTA 1560
QY 1846 CCCTTTGCTCAGGTTCTCCAACTGAGAGAAACCTCTCTGATCTTAGTAGGCTTGA 1902
DB 1561 CCCTTTGCTCAGGTTCTCCAACTGAGAGAAACCTCTCTGATCTTAGTAGGCTTGA 1617

RESULT 5
ADN11979
ID ADN11979 standard; DNA; 1614 BP.
XX
AC ADN11979;
XX
DT 17-JUN-2004 (first entry)
XX
DE Wild type AtNHX1 encoding sequence.
XX
KW salt tolerance; Na+/H+ transporter polypeptide; AtNHX1; ds.
XX
OS Arabidopsis thaliana.
XX

Key Location/Qualifiers
CDS 1..1614
/*tag= a
/product= "AtNHX1"

WO2004007668-A2.

22-JAN-2004.

09-JUL-2003; 2003WO-US021549.

12-JUL-2002; 2002US-0395662P.

(REGC) UNIV CALIFORNIA.

Shi H, Blumwald E;

WPI: 2004-122911/12.

P-PSDB; ADN11980.

Enhancing salt tolerance of a plant comprises introducing into the plant a polynucleotide encoding a Na⁺/H⁺ transporter polypeptide.

Disclosure; SEQ ID NO 1; 38pp; English.

The present invention relates to enhancing salt tolerance of a plant comprises introducing into the plant a polynucleotide encoding a Na⁺/H⁺ transporter polypeptide. The AtNHX1 gene confers salt tolerance. The composition and methods are useful in conferring salt, tolerance on plants and other organisms. The present sequence represents wild type AtNHX1 encoding sequence.

Sequence 1614 BP; 388 A; 346 C; 358 G; 522 T; 0 U; 0 Other;

Query Match 74.1%; Score 1614; DB 12; Length 1614;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1614; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 286 ATGTTGGATTCTCTAGTGTGCAAACTGCTGTTATCGACATCTGATCAGCTTCTGTG 345

DB 1 ATGTTGGATTCTCTAGTGTGCAAACTGCTGTTATCGACATCTGATCAGCTTCTGTG 60

QY 346 GTTGGTGAATCTCTTTGTTGCACTCTTTGTGCTGTTATGTTCTTTGGTCACTTTTG 405

DB 61 GTTGGTGAATCTCTTTGTTGCACTCTTTGTGCTGTTATGTTCTTTGGTCACTTTTG 120

QY 406 GAAGAGATAGATGATGAACGAATCCATCAGCGCTTGTGATGGCTAGGCACTGGT 465

DB 121 GAAGAGATAGATGATGAACGAATCCATCAGCGCTTGTGATGGCTAGGCACTGGT 180

QY 466 GTTACCAATTTGTGATTAGTAAAGGAAAAAGCTCGCATCTCTCGTCTTTAGTGAAGAT 525

DB 181 GTTACCAATTTGTGATTAGTAAAGGAAAAAGCTCGCATCTCTCGTCTTTAGTGAAGAT 240

QY 526 CTTTCTTCATATATCTTTTGGCCCACTTATATTCAATGCAAGGGTTTCAAGTAAAAAG 585

DB 241 CTTTCTTCATATATCTTTTGGCCCACTTATATTCAATGCAAGGGTTTCAAGTAAAAAG 300

QY 586 AAGCAGTTTTCCGCAATTTGCTGACTATTATGCTTTTGGTCTGTTGGGACTATTATT 645

DB 301 AAGCAGTTTTCCGCAATTTGCTGACTATTATGCTTTTGGTCTGTTGGGACTATTATT 360

QY 646 TCTTGCACATCATATCTTAGTGTAAACAGATTTCTTTAAGAGTGTGACATTGGGAACC 705

DB 361 TCTTGCACATCATATCTTAGTGTAAACAGATTTCTTTAAGAGTGTGACATTGGGAACC 420

QY 706 TTTGACTTTGGGTGATTTATCTTGCTATTGTTGTCATATTGCTGCAACAGATTTCAGTATGT 765

DB 421 TTTGACTTTGGGTGATTTATCTTGCTATTGTTGTCATATTGCTGCAACAGATTTCAGTATGT 480

QY 766 ACATGCAAGTTCTGAATCAAGACAGACACCTTTGCTTTACGTCCTTTGATTCGGAGAG 825

DB 481 ACATGCAAGTTCTGAATCAAGACAGACACCTTTGCTTTACGTCCTTTGATTCGGAGAG 540

QY 826 GGTGTGTGAATGATGCAACGTCAGTGTGTGTTCTTCAACGCGATTCAGAGCTTTGATCTC 885

DB 541 GGTGTGTGAATGATGCAACGTCAGTGTGTGTTCTTCAACGCGATTCAGAGCTTTGATCTC 600

QY 886 ACTCACTAAACCAAGAGCTGCTTTTCACTTTCTTTGGAACCTTCTTGTATTTGTTCTC 945

DB 601 ACTCACTAAACCAAGAGCTGCTTTTCACTTTCTTTGGAACCTTCTTGTATTTGTTCTC 660

QY 946 CTAAAGTACCTTGTGTTGCTGCAACCGTCTGATAAGTGGGTATGTTATCAAGAGCTA 1005

DB 661 CTAAAGTACCTTGTGTTGCTGCAACCGTCTGATAAGTGGGTATGTTATCAAGAGCTA 720

QY 1006 TACTTTTGAAGGCACTCAACTGACCGAGAGGTTCCTTTATGATGCTTTATGCGGTATCTT 1065

DB 721 TACTTTTGAAGGCACTCAACTGACCGAGAGGTTCCTTTATGATGCTTTATGCGGTATCTT 780

QY 1066 TCTTATATGCTTGTGAGCTTTTTCGACTTTGAGCGGTATCTTCACTGTTGTTTCTGTG 1125

DB 781 TCTTATATGCTTGTGAGCTTTTTCGACTTTGAGCGGTATCTTCACTGTTGTTTCTGTG 840

QY 1126 ATTGTGATGTCCTTACATGTCACAAATGTAAACGAGAGCTCAAGATTAACACAAAG 1185

DB 841 ATTGTGATGTCCTTACATGTCACAAATGTAAACGAGAGCTCAAGATTAACACAAAG 900

QY 1186 CATACCTTTGCAACTTTTGTCACTTTTTCGCGAGACATTTATTTTCTGTATGTTGGAATG 1245

DB 901 CATACCTTTGCAACTTTTGTCACTTTTTCGCGAGACATTTATTTTCTGTATGTTGGAATG 960

QY 1246 GATGCTTTGGACATTTGACAACTGAGATCCGTGAGTGACACACCGGGAACATTCGATCGCA 1305

DB 961 GATGCTTTGGACATTTGACAACTGAGATCCGTGAGTGACACACCGGGAACATTCGATCGCA 1020

QY 1306 GTGAGCTCAATCTTAATGGGTCTGTCATGTTTTCGAGAGAGAGCGTTTCGTTCCGTTA 1365

DB 1021 GTGAGCTCAATCTTAATGGGTCTGTCATGTTTTCGAGAGAGAGCGTTTCGTTCCGTTA 1080

QY 1366 TCGTTTCTATCTAACTTAGCCAAAGAAATCAAAAGCGAGAAATCAACTTTTAAACATGCA 1425

DB 1081 TCGTTTCTATCTAACTTAGCCAAAGAAATCAAAAGCGAGAAATCAACTTTTAAACATGCA 1140

QY 1426 GTTGTGATTTGGTGTCTGCTCATGAGAGGTGCTGATCTATGGTCTTTGTCATACAAAC 1485

DB 1141 GTTGTGATTTGGTGTCTGCTCATGAGAGGTGCTGATCTATGGCTCTTTGTCATACAAAC 1200

QY 1486 AAGTTTACAGGGCGGGGACACAGATGTACCGGGGATGCAATCATGATCAAGAGTACG 1545

DB 1201 AAGTTTACAGGGCGGGGACACAGATGTACCGGGGATGCAATCATGATCAAGAGTACG 1260

QY 1546 ATAACTGTCTCTTTTGTAGCAGAGTGTGTTTGTGATGCTGACCCAAACCACTCATTAAGC 1605

DB 1261 ATAACTGTCTCTTTTGTAGCAGAGTGTGTTTGTGATGCTGACCCAAACCACTCATTAAGC 1320

QY 1606 TACTTATTAACCGACACGAGCGCCACACGAGCATGTTATCTGATGACAAACCCCAAAA 1665

DB 1321 TACTTATTAACCGACACGAGCGCCACACGAGCATGTTATCTGATGACAAACCCCAAAA 1380

QY 1666 TCCATACATATCCCTTTTGGACCAAGACTCGTTTCATTTGAGCTTTCAGGGAAACCAAT 1725

DB 1381 TCCATACATATCCCTTTTGGACCAAGACTCGTTTCATTTGAGCTTTCAGGGAAACCAAT 1440

QY 1726 GTGCTCGGCTGACAGTATACGTGGCTTCTTGACACGCGCCCACTTCGAAACCGTGCATTAC 1785

DB 1441 GTGCTCGGCTGACAGTATACGTGGCTTCTTGACACGCGCCCACTTCGAAACCGTGCATTAC 1500

QY 1786 TACTGGAGACAAATTTGATGACTCTTTCATGCGACCCGCTTTTGGAGGTGCTGGCTTTGTA 1845

DB 1501 TACTGGAGACAAATTTGATGACTCTTTCATGCGACCCGCTTTTGGAGGTGCTGGCTTTGTA 1560

QY 1846 CCCTTTGTTCCAGGTCTTCCAACTGAGAGAAACCTCTCTGATCTTTAGTAGGCT 1899

DB 1561 CCCTTTGTTCCAGGTCTTCCAACTGAGAGAAACCTCTCTGATCTTTAGTAGGCT 1614

Db 1441 GTGCTCGCCCTGACAGTATACGTGGCTTCTTTGACACGCCCACTCGAACCGTGCATTAC 1500
Qy 1786 TACTGAGACAAATTTGATGACTCTTTCATGCGACCGCTTTGGAGGTGCTGGCTTTGTA 1845
Db 1501 TACTGGAGACAAATTTGATGACTGCTTTCATGCGACCGCTTTGGAGGTGCTGGCTTTGTA 1560
Qy 1846 CCCTTTGTTCCAGGTTCTCCAACTGAGAGAAACCTCTCTGATCTTTAGTAAGGCT 1899
Db 1561 CCCTTTGTTCCAGGTTCTCCAACTGAGAGAAACCTCTCTGATCTTTAGTAAGGCT 1614

RESULT 7
ADN11983
ID ADN11983 standard; DNA; 1563 BP.
XX
AC
XX
ADN11983;
XX
DT 17-JUN-2004 (first entry)
XX
DE AthNX1 mutant encoding sequence #2.
XX
KW salt tolerance; Na+/H+ transporter polypeptide; AtNHX1; ds.
XX
OS Synthetic.
XX
WO2004007668-A2.
XX
PN 22-JAN-2004.
XX
PF 09-JUL-2003; 2003WO-US021549.
XX
PR 12-JUL-2002; 2002US-0395662P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Shi H, Blumwald E;
XX
DR WPI; 2004-122911/12.
DR P-PSDB; ADN11984.
XX
PT Enhancing salt tolerance of a plant comprises introducing into the plant
PT a polynucleotide encoding a Na+/H+ transporter polypeptide.
XX
PS Claim 2; SEQ ID NO 5; 38pp; English.
XX
CC The present invention relates to enhancing salt tolerance of a plant
CC comprises introducing into the plant a polynucleotide encoding a Na+/H+
CC transporter polypeptide. The AtNHX1 gene confers salt tolerance. The
CC composition and methods are useful in conferring salt tolerance on plants
CC and other organisms. The present sequence represents a mutant AtNHX1
CC encoding sequence.
XX
SQ Sequence 1563 BP; 376 A; 333 C; 348 G; 506 T; 0 U; 0 Other;

Query Match : 71.8%; Score 1563; DB 12; Length 1563;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 286 ATGTGGATCTCTAGTGTGGAACCTGCTTGTATGACATCTGATGACGCTTCTGTG 345
Db 1 ATGTGGATCTCTAGTGTGGAACCTGCTTGTATGACATCTGATGACGCTTCTGTG 60

Qy 346 GTTGGTGAATCTTTTGTGACCTTCTTGTGCTTGTATGTTCTTGGTCATCTTTG 405
Db 61 GTTGGTGAATCTTTTGTGACCTTCTTGTGCTTGTATGTTCTTGGTCATCTTTG 120

Qy 406 GAAGAGATAGATGATGAACCAATCCATCCCGCTTGTGATTTGGGTAGGCACTGGT 465
Db 121 GAAGAGATAGATGATGAACCAATCCATCCCGCTTGTGATTTGGGTAGGCACTGGT 180

Qy 466 GTTACATTTTGTGATTAAGAAAAAGCTCGCATCTTCTGTCTTTAGTGAAGAT 525
Db 181 GTTACATTTTGTGATTAAGAAAAAGCTCGCATCTTCTGTCTTTAGTGAAGAT 240

Qy 526 CTTTTCTTATATATCTTTTGGCCACCCATTATATTAATGAGGGTTTCAAGTAAAAAG 585
Db 241 CTTTTCTTATATATCTTTTGGCCACCCATTATATTAATGAGGGTTTCAAGTAAAAAG 300
Qy 586 AAGCAGTTTTTCCGCAATTTTCGTGACTATTAATGCTTTTTTGGTGTGTTGGGACTATATT 645
Db 301 AAGCAGTTTTTCCGCAATTTTCGTGACTATTAATGCTTTTTTGGTGTGTTGGGACTATATT 360
Qy 646 TCTTGCACAATCATATCTCTAGGTGTACACAGTTCTTTTAAGNAGTTGACATTTGGAACC 705
Db 361 TCTTGCACAATCATATCTCTAGGTGTACACAGTTCTTTTAAGNAGTTGACATTTGGAACC 420
Qy 706 TTTGACTTTGGGTGATTTATCTTTGCTATTGCTGCCATATTTGCTGCAACAGATTTCAGTATGT 765
Db 421 TTTGACTTTGGGTGATTTATCTTTGCTATTGCTGCCATATTTGCTGCAACAGATTTCAGTATGT 480
Qy 766 ACATGCAAGTTCTGAATCAAGACGAGACACCTTTGCTTTTACAGTCTTTGTATTCGAGAG 825
Db 481 ACATGCAAGTTCTGAATCAAGACGAGACACCTTTGCTTTTACAGTCTTTGTATTCGAGAG 540
Qy 826 GGTGTTGTAATGATGCAACGTCAGTTGCTGCTTCAACGCGATTTCAGAGCTTTGATCTC 885
Db 541 GGTGTTGTAATGATGCAACGTCAGTTGCTGCTTCAACGCGATTTCAGAGCTTTGATCTC 600
Qy 886 ACTCACCTAAACACGAGAGCTGCTTTTCATCTTTTGGAAAACCTTCTGTTATTTGTTCTC 945
Db 601 ACTCACCTAAACACGAGAGCTGCTTTTCATCTTTTGGAAAACCTTCTGTTATTTGTTCTC 660
Qy 946 CTAAGTACCTTGTGTTGCTGCAACCGGTCGTAAAGTGGTATGTTTATCAAGAAGCTA 1005
Db 661 CTAAGTACCTTGTGTTGCTGCAACCGGTCGTAAAGTGGTATGTTTATCAAGAAGCTA 720
Qy 1006 TACTTTGGAAGGCACTCAACTGACGAGAGGTTGCCCTTATGATGCTTTATGGCGTATCTT 1065
Db 721 TACTTTGGAAGGCACTCAACTGACGAGAGGTTGCCCTTATGATGCTTTATGGCGTATCTT 780
Qy 1066 TCTTATATGCTTGTGAGCTTTTTCGACTTGTAGCGGTATCTCTCACTGTGTTTCTGTGGT 1125
Db 781 TCTTATATGCTTGTGAGCTTTTTCGACTTGTAGCGGTATCTCTCACTGTGTTTCTGTGGT 840
Qy 1126 ATTGTGATGTCCCAATTACATATGACCAATGTAAACGAGAGCTCAAGAAATCAACAAG 1185
Db 841 ATTGTGATGTCCCAATTACATATGACCAATGTAAACGAGAGCTCAAGAAATCAACAAG 900
Qy 1186 CATACCTTTGCAACTTTTGTCAATTTTTCGCGAGACATTTATTTCTGTATGTTGGATG 1245
Db 901 CATACCTTTGCAACTTTTGTCAATTTTTCGCGAGACATTTATTTCTGTATGTTGGATG 960
Qy 1246 GATGCTTTGGAACATTTGCAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA 1305
Db 961 GATGCTTTGGAACATTTGCAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA 1020
Qy 1306 GTGAGCTCAATCTTAATGGGTCTGCTCATGATGAGAGAGCGGCTTCGTTCCGTTA 1365
Db 1021 GTGAGCTCAATCTTAATGGGTCTGCTCATGATGAGAGAGCGGCTTCGTTCCGTTA 1080
Qy 1366 TCGTTTCTATCTAATAGCCCAAGAGATCAAGAGCGAAGAAATCAACTTTAAACATGAG 1425
Db 1081 TCGTTTCTATCTAATAGCCCAAGAGATCAAGAGCGAAGAAATCAACTTTAAACATGAG 1140
Qy 1426 GTTGTGATTTTGGTGTGCTCATGAGAGGTGCTGTATCTATGGCTTCTTGCATACAC 1485
Db 1141 GTTGTGATTTTGGTGTGCTCATGAGAGGTGCTGTATCTATGGCTTCTTGCATACAC 1200
Qy 1486 AAGTTTACAAGGCGCGGCGCACACAGATGTACCGGGAAATGCAATCATGATCAAGATACG 1545
Db 1201 AAGTTTACAAGGCGCGGCGCACACAGATGTACCGGGAAATGCAATCATGATCAAGATACG 1260
Qy 1546 ATAAGTGTCTCTTTTGTAGCACAGTGGTGTGTTGTTGCTGACCAACCACTCATAGC 1605
Db 1261 ATAAGTGTCTCTTTTGTAGCACAGTGGTGTGTTGTTGCTGACCAACCACTCATAGC 1320

QY 1606 TACCTATTACCGCACCAGAACGCCACCGAGCATGTTATCTGATGACAAACACCCCAAAA 1665
DB |||||||
QY 1321 TACCTATTACCGCACCAGAACGCCACCGAGCATGTTATCTGATGACAAACCCCAAAA 1380
DB |||||||
QY 1666 TCCATACATATCCCTTTGTTGGACCAAGACTCGTTTCATTGAGCCCTTCAGGGAACACCAAT 1725
DB |||||||
QY 1381 TCCATACATATCCCTTTGTTGGACCAAGACTCGTTTCATTGAGCCCTTCAGGGAACCAAT 1440
DB |||||||
QY 1726 GTGCTCGGCTGACAGTATACGTGGCTTCTTGACACGCGCCACATCGAACCGTGCAATAC 1785
DB |||||||
QY 1441 GTGCTCGGCTGACAGTATACGTGGCTTCTTGACACGCGCCACATCGAACCGTGCAATAC 1500
DB |||||||
QY 1786 TACTGGAGCAATTTGATGACTCCTTCATGGACCGCTCTTGGAGTCTGGCTTTGTA 1845
DB |||||||
QY 1501 TACTGGAGCAATTTGATGACTCCTTCATGGACCGCTCTTGGAGTCTGGCTTTGTA 1560
DB |||||||
QY 1846 CCC 1848
DB |||
QY 1561 CCC 1563
DB |||
RESULT 8
ADN11989
ID ADN11989 standard; cDNA; 1566 BP.
XX
AC ADN11989;
XX
DT 17-JUN-2004 (first entry)
XX
DE ND1-1 encoding sequence.
XX
KW salt tolerance; Na+/H+ transporter polypeptide; AtNHX1; ss.
XX
OS Saccharomyces sp.
XX
PN WO2004007668-A2.
XX
PD 22-JAN-2004.
XX
PF 09-JUL-2003; 2003WO-US021549.
XX
PR 12-JUL-2002; 2002US-0395662P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Shi H, Blumwald E;
XX
DR WPI; 2004-122911/12.
XX
PS P-PSDB; ADN11990.
XX
PT Enhancing salt tolerance of a plant comprises introducing into the plant
a polynucleotide encoding a Na+/H+ transporter polypeptide.
XX
PS Claim 2; SEQ ID NO 11; 38pp; English.
XX
CC The present invention relates to enhancing salt tolerance of a plant
comprises introducing into the plant a polynucleotide encoding a Na+/H+
transporter polypeptide. The AtNHX1 gene confers salt tolerance. The
composition and methods are useful in conferring salt tolerance on plants
and other organisms. The present sequence represents ND1-1 encoding
sequence.
XX
SQ Sequence 1566 BP; 378 A; 334 C; 349 G; 505 T; 0 U; 0 Other;
Query Match 71.8%; Score 1563; DB 12; Length 1566;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 337 GCTTCTGCTGGTTCGCTTGAATCTCTTGTGACACTCTTGTGCTGCTGCTGCTTCTTGGT 396
DB |||||||
QY 4 GCTTCTGCTGGTTCGCTTGAATCTCTTGTGACACTCTTGTGCTGCTGCTGCTTCTTGGT 63
DB |||||||
QY 397 CATCTTTTGGAGAGAAATAGATGGATGAACGAATCCATCACCGCTTGTGATTGGGCTA 456
DB |||||||

DB |||||||
QY 64 CATCTTTTGGAGAGAAATAGATGGATGAACGAATCCATCACCGCTTGTGATTGGGCTA 123
DB |||||||
QY 457 GGCACTGGTGTACCAATTTTGTGATTAGTAAGGAAAAAGCTCGCATCTTCTCGTCTTT 516
DB |||||||
QY 124 GGCACTGGTGTACCAATTTTGTGATTAGTAAGGAAAAAGCTCGCATCTTCTCGTCTTT 183
DB |||||||
QY 517 AGTGAAGATCTTTTCTTCATATATCTTTTGGCAACCAATATATCAATGCAAGGGTTTCAA 576
DB |||||||
QY 184 AGTGAAGATCTTTTCTTCATATATCTTTTGGCAACCAATATATCAATGCAAGGGTTTCAA 243
DB |||||||
QY 577 GTAAAAAAGAGCAGTCTTTTCCGCAATTTCTGCTACTATATGCTTTTGGTCTGTTGGG 636
DB |||||||
QY 244 GTAAAAAAGAGCAGTCTTTTCCGCAATTTCTGCTACTATATGCTTTTGGTCTGTTGGG 303
DB |||||||
QY 637 ACTATTATTTCTTGCACAATCATATCTCTAGGTGTAAACACAGATTTCTTTAAGAAGTTGGAC 696
DB |||||||
QY 304 ACTATTATTTCTTGCACAATCATATCTCTAGGTGTAAACACAGATTTCTTTAAGAAGTTGGAC 363
DB |||||||
QY 697 ATTGGAACCTTTGACTTGGGTGATATCTTGCTATTTGGTGCATATTTGCTGCAACAGAT 756
DB |||||||
QY 364 ATTGGAACCTTTGACTTGGGTGATATCTTGCTATTTGGTGCATATTTGCTGCAACAGAT 423
DB |||||||
QY 757 TCAGTATGTACACTGCAGGTTCTGAATCAAGACGACACCTTTGCTTTACAGTCTTGTGA 816
DB |||||||
QY 424 TCAGTATGTACACTGCAGGTTCTGAATCAAGACGACACCTTTGCTTTACAGTCTTGTGA 483
DB |||||||
QY 817 TTGGAGAGGGTGTGTGAATGATGCAACGTCAGTGTGTGTCCTTCAACGCGATTCAGAGC 876
DB |||||||
QY 484 TTGGAGAGGGTGTGTGAATGATGCAACGTCAGTGTGTGTCCTTCAACGCGATTCAGAGC 543
DB |||||||
QY 877 TTTGATCTCACTCACTAAACCAAGAGCTCTTTTTCATCTTCTTGGAACTCTTCTGTAT 936
DB |||||||
QY 544 TTTGATCTCACTCACTAAACCAAGAGCTCTTTTTCATCTTCTTGGAACTCTTCTGTAT 603
DB |||||||
QY 937 TTGTTTCTCTTAAGTACCTTCTGCTGTCGCAACGCTCTGATAAGTGCCTATGTTATC 996
DB |||||||
QY 604 TTGTTTCTCTTAAGTACCTTCTGCTGTCGCAACGCTCTGATAAGTGCCTATGTTATC 663
DB |||||||
QY 997 AAGAACTATATCTTTTGAAGGCACTCAACTGACCGAGAGGTTGCCCTTATGATCTTATG 1056
DB |||||||
QY 664 AAGAACTATATCTTTTGAAGGCACTCAACTGACCGAGAGGTTGCCCTTATGATCTTATG 723
DB |||||||
QY 1057 GCGTATCTTTCTTATATGCTGCTGAGCTTTTCACTTGGCGGTATCTTCACTGTGTTT 1116
DB |||||||
QY 724 GCGTATCTTTCTTATATGCTGCTGAGCTTTTTCGACTTGAAGCGGTATCTTCACTGTGTT 783
DB |||||||
QY 1117 TTCTGTGTATTGTGATGTCCTTACATGCGCACAAATGTAAACGGAGAGCTCAAGAATA 1176
DB |||||||
QY 784 TTCTGTGTATTGTGATGTCCTTACATGCGCACAAATGTAAACGGAGAGCTCAAGAATA 843
DB |||||||
QY 1177 ACAACAAAGCATACCTTTGCAACTTTTGTCAATTTCTTGGGAGACATTTATTTTCTTGTAT 1236
DB |||||||
QY 844 ACAACAAAGCATACCTTTGCAACTTTTGTCAATTTCTTGGGAGACATTTATTTTCTTGTAT 903
DB |||||||
QY 1237 GTTGGAAATGATGCTTTGGCAATTTGCAAGTGGAGATCCGTGAGTGACACACCGGACACA 1296
DB |||||||
QY 904 GTTGGAAATGATGCTTTGGCAATTTGCAAGTGGAGATCCGTGAGTGACACACCGGGAACA 963
DB |||||||
QY 1297 TCGATCGCAGTGAGCTCAATCTCTAATGGGCTCTGCTCATGTTGGAAAGACGAGCTTCGTC 1356
DB |||||||
QY 964 TCGATCGCAGTGAGCTCAATCTCTAATGGGCTCTGCTCATGTTGGAAAGACGAGCTTCGTC 1023
DB |||||||
QY 1357 TTTCCGTTATCGTTTCTTATCTAACTTAGCCAAAGAAATCAAACGGAGAAATCAACTTTT 1416
DB |||||||
QY 1024 TTTCCGTTATCGTTTCTTATCTAACTTAGCCAAAGAAATCAAACGGAGAAATCAACTTTT 1083
DB |||||||
QY 1417 AACATGCAAGTTGCTGATTTGGTGTCTGCTCTCATGAGAGTGTCTGTATCTATCGCTCTT 1476
DB |||||||
QY 1084 AACATGCAAGTTGCTGATTTGGTGTCTGCTCTCATGAGAGTGTCTGTATCTATCGCTCTT 1143
DB |||||||
QY 1477 GCATACAAAGTTTACAAAGGGCCGGGACACACATGTACCGGGAATGCAATCATGATC 1536
DB |||||||

Db 1144 GCATCAACAAGTTTACAAAGCGCGGCACACAGATGTACGCGGAATGCAATCATGATC 1203
QY 1537 ACAGTACGATACATCTGTCTCTTTTATGACACAGTGGTGTGGTATGCTGACCAACCA 1596
Db 1204 ACAGTACGATACATCTGTCTCTTTTATGACACAGTGGTGTGGTATGCTGACCAACCA 1263
QY 1597 CTCATAAGTACTATTAACCGCACAGAACCGCAACAGAGCATGTTATCTGATGACAAC 1656
Db 1264 CTCATAAGTACTATTAACCGCACAGAACCGCAACAGAGCATGTTATCTGATGACAAC 1323
QY 1657 ACCCCAAATCCATACATATCCCTTTGTGGACCAAGACTGCTTCATTTGAGCCCTCAGG 1716
Db 1324 ACCCCAAATCCATACATATCCCTTTGTGGACCAAGACTGCTTCATTTGAGCCCTCAGG 1383
QY 1717 AACCAATATGCTCGGCTGACAGTATACGTGCTCTTTCGACACGGCCCACTCGAAC 1776
Db 1384 AACCAATATGCTCGGCTGACAGTATACGTGCTCTTTCGACACGGCCCACTCGAAC 1443
QY 1777 GTGCATTAATCTAGTACGACAAATTTGATGACTCTCTTCATGCGACCCGCTTTTGGAGTCT 1836
Db 1444 GTGCATTAATCTAGTACGACAAATTTGATGACTCTCTTCATGCGACCCGCTTTTGGAGTCT 1503
QY 1837 GCCTTTGTACCTTTGTTCCAGTTCTCCAACTGAGAGAAACCTCTCTGATCTTAGTAAG 1896
Db 1504 GCCTTTGTACCTTTGTTCCAGTTCTCCAACTGAGAGAAACCTCTCTGATCTTAGTAAG 1563
QY 1897 GCT 1899
Db 1564 GCT 1566

RESULT 9

ADN11985
ID ADN11985 standard; DNA; 1473 BP.
XX
AC ADN11985;
XX
DT 17-JUN-2004 (first entry)
XX
DE AtNHX1 mutant encoding sequence #3.
XX
KW salt tolerance; Na+/H+ transporter polypeptide; AtNHX1; ds.
XX
OS Synthetic.
XX
PN WO2004007668-A2.
XX
PD 22-JAN-2004.
XX
PF 09-JUL-2003; 2003WO-US021549.
XX
PR 12-JUL-2002; 2002US-0395662P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Shi H, Blumwald E;
XX
DR WPI; 2004-122911/12.
DR P-FSDB; ADN11986.
XX
PT Enhancing salt tolerance of a plant comprises introducing into the plant
PT a polynucleotide encoding a Na+/H+ transporter polypeptide.
XX
PS Claim 4; SEQ ID NO 7; 38pp; English.
XX
CC The present invention relates to enhancing salt tolerance of a plant
CC comprises introducing into the plant a polynucleotide encoding a Na+/H+
CC transporter polypeptide. The AtNHX1 gene confers salt tolerance. The
CC composition and methods are useful in conferring salt tolerance on plants
CC and other organisms. The present sequence represents a mutant AtNHX1
CC encoding sequence.
XX
SQ Sequence 1473 BP; 358 A; 306 C; 327 G; 482 T; 0 U; 0 Other;

		Query Match		67.6%; Score 1473; DB 12; Length 1473;		Best Local Similarity 100.0%; Pred. No. 0;		Matches 1473; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	286	ATGTTGGATCTCTAGTGTGCAAACTGCTTCGTTATCGACATCTGATCAGCCTTCTGTG	345						
Db	1	ATGTTGGATCTCTAGTGTGCAAACTGCTTCGTTATCGACATCTGATCAGCCTTCTGTG	60						
QY	346	GTTGGTTGAATCTCTTTGTTGCACTTCTTTGTGCTGTTATTTGTTCTTGGTTCATCTTTG	405						
Db	61	GTTGGTTGAATCTCTTTGTTGCACTTCTTTGTGCTGTTATTTGTTCTTGGTTCATCTTTG	120						
QY	406	GAAGAGATAGATGGATGCAAGATCCATCACCGCTTTGTTGATTTGGGTAGGCACTGCT	465						
Db	121	GAAGAGATAGATGGATGCAAGATCCATCACCGCTTTGTTGATTTGGGTAGGCACTGCT	180						
QY	466	GTTACCATTTTGGTGAATAGTAAAGGAAAAAGCTCGCATCTTCTCGTCTTTAGTGAAGAT	525						
Db	181	GTTACCATTTTGGTGAATAGTAAAGGAAAAAGCTCGCATCTTCTCGTCTTTAGTGAAGAT	240						
QY	526	CTTTTCTTCATATATCTTTTCCGCAATTTGCTGACTATTTGCTTTTGGTGTCTTGGGACTAT	585						
Db	241	CTTTTCTTCATATATCTTTTCCGCAATTTGCTGACTATTTGCTTTTGGTGTCTTGGGACTAT	300						
QY	586	AAGCAGTTTTCGCAATTTGCTGACTATTTGCTTTTGGTGTCTTGGGACTATTTAT	645						
Db	301	AAGCAGTTTTCGCAATTTGCTGACTATTTGCTTTTGGTGTCTTGGGACTATTTAT	360						
QY	646	TCTTGCACAATATCTCTAGGTGTAACAAGTTCTTTTAAAGAGTTGGACATTTGGAACC	705						
Db	361	TCTTGCACAATATCTCTAGGTGTAACAAGTTCTTTTAAAGAGTTGGACATTTGGAACC	420						
QY	706	TTTGACTTGGGTGATATCTTCTATTTGGTGCCATTTTGTGCTGCTTGTGCAACAGATTCAG	765						
Db	421	TTTGACTTGGGTGATATCTTCTATTTGGTGCCATTTTGTGCTGCTTGTGCAACAGATTCAG	480						
QY	766	ACACTGCAAGTTCTGAATCAAGACGAGACACCTTTTGTCTTTACAGTCTTGTATTCGGAGAG	825						
Db	481	ACACTGCAAGTTCTGAATCAAGACGAGACACCTTTTGTCTTTACAGTCTTGTATTCGGAGAG	540						
QY	826	GCTGTGTGAATGATGCAACCTGCTGCTTCTTCAACCGGATTCAGAGCTTTGATCTC	885						
Db	541	GCTGTGTGAATGATGCAACCTGCTGCTTCTTCAACCGGATTCAGAGCTTTGATCTC	600						
QY	886	ACTCACCTAAACACGAGCTGCTTTTCATCTTCTTGGAACTTCTCTTATTTGTTCTC	945						
Db	601	ACTCACCTAAACACGAGCTGCTTTTCATCTTCTTGGAACTTCTCTTATTTGTTCTC	660						
QY	946	CTAAGTACCTTTGCTTGGTGTGCAACCGGTCTGATAAGTGGGTATGTTATCAAGAAAGCTA	1005						
Db	661	CTAAGTACCTTTGCTTGGTGTGCAACCGGTCTGATAAGTGGGTATGTTATCAAGAAAGCTA	720						
QY	1006	TACTTTGGAAGGCACTCAACTGACGAGAGTGTGCTTATGATGCTTATGCGGTATCTT	1065						
Db	721	TACTTTGGAAGGCACTCAACTGACGAGAGTGTGCTTATGATGCTTATGCGGTATCTT	780						
QY	1066	TCCTATATGCTTGTGAGCTTTTCGACTTGGAGCGGTATCCTCACTGCTGTTTCTGTGCT	1125						
Db	781	TCCTATATGCTTGTGAGCTTTTCGACTTGGAGCGGTATCCTCACTGCTGTTTCTGTGCT	840						
QY	1126	ATTGTGATGTCCCATTTACACATGGCACAATGTAAACGGAGAGCTCAAGAAATCAACAAG	1185						
Db	841	ATTGTGATGTCCCATTTACACATGGCACAATGTAAACGGAGAGCTCAAGAAATCAACAAG	900						
QY	1186	CATACCTTTGCAACTTTGTCTATTTCTTCGGAGACATTTATTTCTTGTATGTTGGAATG	1245						
Db	901	CATACCTTTGCAACTTTGTCTATTTCTTCGGAGACATTTATTTCTTGTATGTTGGAATG	960						
QY	1246	GATGCTTGGACATTTGACAAAGTGGAGATCCCTGAGTGAACACCGGGAAACATCGATCGCA	1305						
Db	961	GATGCTTGGACATTTGACAAAGTGGAGATCCCTGAGTGAACACCGGGAAACATCGATCGCA	1020						

Qy 1306 GTGAGCTCAATCCTAATGGGTCTGTCATGTTGGAGAGCAGCGTTCGTCTTCCGTTA 1365
Db |||||||
Qy 1021 GTGAGCTCAATCCTAATGGGTCTGTCATGTTGGAGAGCAGCGTTCGTCTTCCGTTA 1080
Db |||||||
Qy 1366 TCGTTTCTATCTAACTTAGCCAAAGAAATCAAAAGCGAGAAAATCAACTTTAAACATGCAG 1425
Db |||||||
Qy 1081 TCGTTTCTATCTAACTTAGCCAAAGAAATCAAAAGCGAGAAAATCAACTTTAAACATGCAG 1140
Qy 1426 GTTGATGATTTGGTGTCTGGTCTCATGAGAGGTGCTGTATCTATGAGTCTTGGCTTTGCATACAAC 1485
Db |||||||
Qy 1141 GTTGTGATTTGGTGTCTGGTCTCATGAGAGGTGCTGTATCTATGGCTCTTGCATACAAC 1200
Qy 1486 AAGTTTCAAGGGCGGGCACACAGATGTACGCGGAATGCAATCATGATCACAGATACG 1545
Db |||||||
Qy 1201 AAGTTTCAAGGGCGGGCACACAGATGTACGCGGAATGCAATCATGATCACAGATACG 1260
Qy 1546 ATAAGTGTCTCTTTTATGACAGAGTGTGTTGGTATGCTGACCAACCACTCATTAAGC 1605
Db |||||||
Qy 1261 ATAAGTGTCTCTTTTATGACAGAGTGTGTTGGTATGCTGACCAACCACTCATTAAGC 1320
Qy 1606 TACCTATTACCGACACAGAGCGCACACAGATGTATCTGATGACAAACACCCCAAAA 1665
Db |||||||
Qy 1321 TACCTATTACCGACACAGAGCGCACACAGATGTATCTGATGACAAACACCCCAAAA 1380
Qy 1666 TCCATACATATCCCTTCTGTCGACCAAGACTCGTTCAATGAGCCTTCAGGGAACCAAT 1725
Db |||||||
Qy 1381 TCCATACATATCCCTTCTGTCGACCAAGACTCGTTCAATGAGCCTTCAGGGAACCAAT 1440
Qy 1726 GTGGCTCGGCTGACAGTATACGTGGCTTCCTTG 1758
Db |||||||
Qy 1441 GTGGCTCGGCTGACAGTATACGTGGCTTCCTTG 1473

RESULT 10

ADN11991
ID ADN11991 standard; cDNA; 1410 BP.
XX
AC ADN11991;
XX
DT 17-JUN-2004 (first entry)
XX
DE NDL-2 encoding sequence.
XX
KW salt tolerance; Na+/H+ transporter polypeptide; AtNHX1; ss.
XX
OS Saccharomyces sp.
XX
FN WO2004007668-A2.
XX
PD 22-JAN-2004.
XX
PF 09-JUL-2003; 2003WO-US021549.
XX
PR 12-JUL-2002; 2002US-0395662P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Shi H, Blumwald E;
XX
DR WPI; 2004-122911/12.
XX
DR P-PSDB; ADN11992.
XX
PT Enhancing salt tolerance of a plant comprises introducing into the plant
a polynucleotide encoding a Na+/H+ transporter polypeptide.
XX
PS Claim 4; SEQ ID NO 13; 38pb; English.
XX
CC The present invention relates to enhancing salt tolerance of a plant
comprises introducing into the plant a polynucleotide encoding a Na+/H+
transporter polypeptide. The AtNHX1 gene confers salt tolerance. The
composition and methods are useful in conferring salt tolerance on plants
and other organisms. The present sequence represents NDL-2 encoding
sequence.

XX SQ Sequence 1410 BP; 348 A; 309 C; 309 G; 444 T; 0 U; 0 Other;
Query Match 64.6%; Score 1407; DB 12; Length 1410;
Best Local Similarity 100.0%; Pred. No. 6.7e-308;
Matches 1407; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 493 AAAAGCTGGCATCTTCTCGTCTTTAGTGAAGATCTTTCTTCATATATCTTTGGCCACCC 552
Db |||||||
Qy 553 ATTATATTCAATGACAGGGTTTCAAGTAAAAAAGACAGTTTTTCCGCAATTTCTGTCAGT 612
Db |||||||
Qy 64 ATTATATTCAATGACAGGGTTTCAAGTAAAAAAGACAGTTTTTCCGCAATTTCTGTCAGT 123
Qy 613 ATTATGCTTTTGGTGTCTGTTGGGACTATTTATTTTTCGCACAATCATATCTCTAGGTGTA 672
Db |||||||
Qy 124 ATTATGCTTTTGGTGTCTGTTGGGACTATTTATTTCTTGGCACAATCATATCTCTAGGTGTA 183
Qy 673 ACACAGTCTTTAAGAAGTTGGACATTTGGAACCTTTTGACTTTGGTGATTAATCTTGTCTATT 732
Db |||||||
Qy 184 ACACAGTCTTTAAGAAGTTGGACATTTGGAACCTTTTGACTTTGGTGATTAATCTTGTCTATT 243
Qy 733 GGTGCCATATTGTCGCAACAGATTCAGTATGTACACTGCAGGTTCTGAATCAAGACGAG 792
Db |||||||
Qy 244 GGTGCCATATTGTCGCAACAGATTCAGTATGTACACTGCAGGTTCTGAATCAAGACGAG 303
Qy 793 ACACCTTTTGTCTTACAGTCTTTGATTCGAGAGGGTGTGTGAATGATGAACGTCAGTT 852
Db |||||||
Qy 304 ACACCTTTTGTCTTACAGTCTTTGATTCGAGAGGGTGTGTGAATGATGAACGTCAGTT 363
Qy 853 GTGGTCTTCAACGGGATTGAGCTTTGATCTCACTCACTTAACACCAAGCTGCTTTT 912
Db |||||||
Qy 364 GTGGTCTTCAACGGGATTGAGCTTTGATCTCACTCACTTAACACCAAGCTGCTTTT 423
Qy 913 CATCTTCTTGAAACTTCTTGTATTTCTCTAAGTACCTTGTCTGTCGCAACC 972
Db |||||||
Qy 424 CATCTTCTTGAAACTTCTTGTATTTCTCTAAGTACCTTGTCTGTCGCAACC 483
Qy 973 GGTCTGATAAGTGGTATGTTATCAAGAAGCTATATTTTGGAGGCACTCAACTGACCGA 1032
Db |||||||
Qy 484 GGTCTGATAAGTGGTATGTTATCAAGAAGCTATATTTTGGAGGCACTCAACTGACCGA 543
Qy 1033 GAGGTTGCCCTTATGATGCTTATGGCGTATCTTCTTATATGCTTGTGAGCTTTTCGAC 1092
Db |||||||
Qy 544 GAGGTTGCCCTTATGATGCTTATGGCGTATCTTCTTATATGCTTGTGAGCTTTTCGAC 603
Qy 1093 TTGAGCGGTATCCCTCACTGTGTTTTCTGTGGTATTTGTGATGTCCTCATACATGGCAC 1152
Db |||||||
Qy 604 TTGAGCGGTATCCCTCACTGTGTTTTCTGTGGTATTTGTGATGTCCTCATACATGGCAC 663
Qy 1153 AATGTAAACGAGAGCTCAAGAAATCAACAAAGATACCTTTTGGCACTTTGTCTATTCTT 1212
Db |||||||
Qy 664 AATGTAAACGAGAGCTCAAGAAATCAACAAAGATACCTTTTGGCACTTTGTCTATTCTT 723
Qy 1213 GCGGAGACATTTATTTTCTGTATGTTGGAATGGATGCTTGGACATTTGCAAGTGAGA 1272
Db |||||||
Qy 724 GCGGAGACATTTATTTTCTGTATGTTGGAATGGATGCTTGGACATTTGCAAGTGAGA 783
Qy 1273 TCCGTGAGTGACACACCGGGAACATCCATCGAGTGAGCTCAATCTTAATGGGTCTGGTC 1332
Db |||||||
Qy 784 TCCGTGAGTGACACACCGGGAACATCCATCGAGTGAGCTCAATCTTAATGGGTCTGGTC 843
Qy 1333 ATGGTTGGAAGAGCAGCGTTTCGTTTCGTTATCGTTTCTATCTAATCTTAGGCAAGAG 1392
Db |||||||
Qy 844 ATGGTTGGAAGAGCAGCGTTTCGTTTCGTTATCGTTTCTATCTAATCTTAGGCAAGAG 903
Qy 1393 AATCAAGCGGAGAAATCAACATTAACATGAGTGTGATTTGGTGTCTGTCATG 1452
Db |||||||
Qy 904 AATCAAGCGGAGAAATCAACATTAACATGAGTGTGATTTGGTGTCTGTCATG 963
Qy 1453 AGAGGTCTGTATCTATGGCTCTTGGCATACAAGTTTACAAGGGCGGGGCAACAGAT 1512
Db |||||||

Db 964 AGAGGTGCTGTAATCTATGCTCTTGCCATACAAAGTTTAAAGGGCGGGCACAGAT 1023
QY 1513 GTACGGGGGAATGCAATCATGATCAGAGTACGATAAAGTCTGCTCTTTTATGACAGTG 1572
Db 1024 GTACGGGGGAATGCAATCATGATCAGAGTACGATAAAGTCTGCTCTTTTATGACAGTG 1083
QY 1573 GTGTTTGGTATGCTGACCAAAACACTCATAAGCTACCTATTACCGCACCAAGCCACC 1632
Db 1084 GTGTTTGGTATGCTGACCAAAACACTCATAAGCTACCTATTACCGCACCAAGCCACC 1143
QY 1633 ACAGCATCTTATCTGTAGTACACACACCCCAAAATCCATACATATCCCTTTGTTGACCA 1692
Db 1144 ACAGCATCTTATCTGTAGTACACACACCCCAAAATCCATACATATCCCTTTGTTGACCA 1203
QY 1693 GACTCGTTCAATGAGGCTTTGAGGAAACCAATGTGCTCGGCTGACAGTATACGTGGC 1752
Db 1204 GACTCGTTCAATGAGGCTTCAGGAAACCAATGTGCTCGGCTGACAGTATACGTGGC 1263
QY 1753 TTCTTGACACGGCCCACTCGAACCGTGCAATTAATCTGAGACAAATTTGATGACTCCTTC 1812
Db 1264 TTCTTGACACGGCCCACTCGAACCGTGCAATTAATCTGAGACAAATTTGATGACTCCTTC 1323
QY 1813 ATGCGACCGCTCTTTGGAGGTGCTGGCTTTGTACCCCTTTGTTCCAGGTTCTCCAAGTG 1872
Db 1324 ATGCGACCGCTCTTTGGAGGTGCTGGCTTTGTACCCCTTTGTTCCAGGTTCTCCAAGTG 1383
QY 1873 AGAAACCCCTCTGATCTTAGTAAGGCT 1899
Db 1384 AGAAACCCCTCTGATCTTAGTAAGGCT 1410

RESULT 11

ADN11987

ID ADN11987 standard; DNA; 1362 BP.

XX AC ADN11987;

XX DT 17-JUN-2004 (first entry)

XX DE AtNHX1 mutant encoding sequence #4.

XX KW salt tolerance; Na+/H+ transporter polypeptide; AtNHX1; ds.

XX OS Synthetic.

XX PN WO2004007668-A2.

XX XX 22-JAN-2004.

XX PF 09-JUL-2003; 2003WO-US021549.

XX PR 12-JUL-2002; 2002US-0395662P.

XX XX (REGC) UNIV, CALIFORNIA.

XX PA Shi H, Blumwald E;

XX PI WPI: 2004-122911/12.

XX DR P-PSDB; ADN11988.

XX XX Enhancing salt tolerance of a plant comprises introducing into the plant

XX PT a polynucleotide encoding a Na+/H+ transporter polypeptide.

XX PS Claim 7; SEQ ID NO 9; 38pp; English.

XX CC The present invention relates to enhancing salt tolerance of a plant

XX CC comprises introducing into the plant a polynucleotide encoding a Na+/H+

XX CC transporter polypeptide. The AtNHX1 gene confers salt tolerance. The

XX CC composition and methods are useful in conferring salt tolerance on plants

XX CC and other organisms. The present sequence represents a mutant AtNHX1

XX CC encoding sequence.

XX XX Sequence 1362 BP; 329 A; 274 C; 305 G; 454 T; 0 U; 0 Other;

XX SQ

Query Match
Best Local Similarity 62.5%; Score 1362; DB 12; Length 1362;
Matches 1362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 286 ATGTTGGATCTCTAGTGTGAAAGTGGCTTCTGTTATCGACATCTGATCAGCTTCTGTG 345
Db 1 ATGTTGGATCTCTAGTGTGAAAGTGGCTTCTGTTATCGACATCTGATCAGCTTCTGTG 60
QY 346 GTTGGGTTGAATCTCTTTGTTGCACTTCTTTGTTGCTGTTATGTTCTTGGTCACTTTTG 405
Db 61 GTTGGGTTGAATCTCTTTGTTGCACTTCTTTGTTGCTGTTATGTTCTTGGTCACTTTTG 120
QY 406 GAAGAGATAGATGGATGAACGAATCCATCACCGCTTGTGTTGTTGTTGTTGTTGTTGTTG 465
Db 121 GAAGAGATAGATGGATGAACGAATCCATCACCGCTTGTGTTGTTGTTGTTGTTGTTGTTG 180
QY 466 GTTACCAATTTTGGTATGTTAGTAAAGGAAAGTGTGCTCTCTGTTCTTCTGTTCTTCTG 525
Db 181 GTTACCAATTTTGGTATGTTAGTAAAGGAAAGTGTGCTCTCTGTTCTTCTGTTCTTCTG 240
QY 526 CTTTCTTTCATATATCTTTTGGCCACCCCAATATATTCATGCAAGGTTTCAAGTAAAG 585
Db 241 CTTTCTTTCATATATCTTTTGGCCACCCCAATATATTCATGCAAGGTTTCAAGTAAAG 300
QY 586 AAGCAGTTTTCGCGCAATTTCTGCTGACTATATGCTTTTGGTGTCTGTTGGGACTATTATT 645
Db 301 AAGCAGTTTTCGCGCAATTTCTGCTGACTATATGCTTTTGGTGTCTGTTGGGACTATTATT 360
QY 646 TCTTGCACAATCATATCTCTAGGTGTAAACAGTTTCTTTAAGAAAGTTCGACATTCGAACC 705
Db 361 TCTTGCACAATCATATCTCTAGGTGTAAACAGTTTCTTTAAGAAAGTTCGACATTCGAACC 420
QY 706 TTTGACTTGGGTGATTATCTTGTCTATTTGTTGCCATATTTGTTGCAACAGATTCAGTATGT 765
Db 421 TTTGACTTGGGTGATTATCTTGTCTATTTGTTGCCATATTTGTTGCAACAGATTCAGTATGT 480
QY 766 ACATGTCAGGTTCTGAATCAAGACGAGACACCTTTGCTTTACAGTCTTGTATTTCGGAGAG 825
Db 481 ACATGTCAGGTTCTGAATCAAGACGAGACACCTTTGCTTTACAGTCTTGTATTTCGGAGAG 540
QY 826 GGTGTTGTAATGATGCAACCTGCTGTTGTTCTTCAACGGGATTCAGAGCTTTCATCTC 885
Db 541 GGTGTTGTAATGATGCAACCTGCTGTTGTTCTTCAACGGGATTCAGAGCTTTCATCTC 600
QY 886 ACTCACCTAAACACGAGCTGCTTTTCATCTTCTTGGAAATCTTCTGTTATTTGTTTCTC 945
Db 601 ACTCACCTAAACACGAGCTGCTTTTCATCTTCTTGGAAATCTTCTGTTATTTGTTTCTC 660
QY 946 CTAAGTACCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1005
Db 661 CTAAGTACCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 720
QY 1006 TACTTTGGAAGGCACTCAACTGACCGAGAGGTTGCCCTTATGATGCTTATGGCGTATCTT 1065
Db 721 TACTTTGGAAGGCACTCAACTGACCGAGAGGTTGCCCTTATGATGCTTATGGCGTATCTT 780
QY 1066 TCTTATATGCTGCTGAGCTTTTTCGATGAGCGGTATCTTCTGCTGTTGTTTCTGTTGTT 1125
Db 781 TCTTATATGCTGCTGAGCTTTTTCGATGAGCGGTATCTTCTGCTGTTGTTTCTGTTGTT 840
QY 1126 ATTGTGATGTCCTCCATTTACATATGCAATGCAATGTAACGGAGAGCTCAAGAAATCAACA 1185
Db 841 ATTGTGATGTCCTCCATTTACATATGCAATGTAACGGAGAGCTCAAGAAATCAACA 900
QY 1186 CATACCTTTGCAACTTTGTGCAATTTCTTGGGAGACATTTATTTCTTGTATGTTGGAAATG 1245
Db 901 CATACCTTTGCAACTTTGTGCAATTTCTTGGGAGACATTTATTTCTTGTATGTTGGAAATG 960
QY 1246 GATGCTTGGACATTTGACAACTGGAGATCCCTGAGTGTGACACACCGGGAAACATCGATCG 1305
Db 961 GATGCTTGGACATTTGACAACTGGAGATCCCTGAGTGTGACACACCGGGAAACATCGATCG 1020

Db 1082 CCCAAATCCATACATATATCCCTTTGTTGGACAAGACATCGTTCAATGAGCCCTCAGGGA 1141
Qy 1718 ACCAATGTGCTCGGCTGACAGTATACGTGGCTTTTGACACGGCCCACTCGAACC 1777
Db 1142 ACCAATGTGCTCGGCTGACAGTATACGTGGCTTTTGACACGGCCCACTCGAACC 1201
Qy 1778 TGAATTAATCTGAGACAAATTTGATGATCTCTTCATGCGACCCGCTTTTGGAGGTCGTG 1837
Db 1202 TGAATTAATCTGAGACAAATTTGATGATCTCTTCATGCGACCCGCTTTTGGAGGTCGTG 1261
Qy 1838 GCTTTGACCCCTTTGTTCCAGGTTCTCCAACTGAGAGAAACCTCTCTGATCTTAGTAAG 1897
Db 1262 GCTTTGACCCCTTTGTTCCAGGTTCTCCAACTGAGAGAAACCTCTCTGATCTTAGTAAG 1321
Qy 1898 CT 1899
Db 1322 CT 1323

RESULT 13
ADM68265
ID ADM68265 standard; DNA; 1449 BP.
XX
AC ADM68265;
XX
DT 03-JUN-2004 (first entry)
XX
DE Plant Na+/H+ antiporter protein gene.
XX
KW ds; gene; salt-resistance; MGX4; mangrove; drought-resistance; plant;
KW transgenic plant; Na+/H+ antiporter protein; NHX1.
XX
OS Unidentified.
XX
PN CN1448511-A.
XX
PD 15-OCT-2003.
XX
PF 02-APR-2002; 2002CN-00111229.
XX
PR 02-APR-2002; 2002CN-00111229.
XX
PA (ZHAN/) ZHANG H.
XX
PI Zhang H;
XX
DR WPI; 2004-091822/10.
XX
PT Salt tolerance gene MGX4 and method of breeding a salt and drought
PT tolerant plant variety.
XX
PS Disclosure; Page 10-12; 19pp; Chinese.
XX
CC The invention relates to a novel salt-resistance gene MGX4 from mangrove
CC or other drought-resistant plant. Breeding a salt and drought resistant
CC plant variety comprises fusing the gene with the forced constitutive
CC expression promoter 35S to generate vector pHXZ. The gene is transfected
CC into a recipient plant by agrobacterium mediated transformation to give a
CC salt and drought tolerant transgenic plant. This sequence corresponds to
CC the DNA encoding a plant MGX4 protein. The sequence is used for
CC comparison with the Arabidopsis thaliana NHX1 gene.
XX
SQ Sequence 1449 BP; 355 A; 326 C; 304 G; 464 T; 0 U; 0 Other;

Query Match 38.9%; Score 848; DB 12; Length 1449;
Best Local Similarity 82.0%; Pred. No. 1.6e-181;
Matches 977; Conservative 0; Mismatches 215; Indels 0; Gaps 0;

Qy 427 GAATCCATCACCCTGTTGTTGATGGCTAGGCACTGGTGTACCATTTTGTGATTAGT 486
Db 198 GATTCCATCACCCTGTTGTTGATGGCTAGGCACTGGTGTACCATTTTGTGATTAGT 257
Qy 487 AAAGGAAAAGCTCGCATCTTCTCGTCTTTAGTGAAGATCTTTTCTCATATATCTTTG 546

Db 258 AAAGGAAAAGCTCGCATCTTCTCGTCTTTAGTGAAGATCTTTTCTCATATATCTTTG 317
Qy 547 CCACCCATTTATTTCAATGCAGGGTTTCAAGTAAAAAAGAGACAGTTCCTCCGCAATTC 606
Db 318 CCACCCATTTATTTCAATGCAGGGTTTCAAGTAAAAAAGAGACAGTTCCTCCGCAATTC 377
Qy 607 GTGACTATATGCTTTTGGTCTCTGTTGGACTATTTATTTCTGCACAAATCATATCTCTA 666
Db 378 GTGACTATATGCTTTTGGTCTCTGTTGGACTATTTATTTCTGCACAAATCATATCTCTA 437
Qy 667 GGTGTAAACACAGTCTTTTAAAGAGTTGACATTTGGAACCTTTGACTTGGGTGATATCTT 726
Db 438 GGTGTAAACACAGTCTTTTAAAGAGTTGACATTTGGAACCTTTGACTTGGGTGATATCTT 497
Qy 727 GCTATTGTTGCCATATTTGCTGCACACAGATTCAGTATGTACACTGCAGGTTCTGATCAA 786
Db 498 GCTATTGTTGCCATATTTGCTGCACACAGATTCAGTATGTACACTGCAGGTTCTGATCAA 557
Qy 787 GACGAGACACCTTTGCTTTTACAGTCTTGTATTTCCGAGAGGGTGTGTGAATGATCAACG 846
Db 558 GACGAGACACCTTTGCTTTTACAGTCTTGTATTTCCGAGAGGGTGTGTGAATGATCAACG 617
Qy 847 TCAGTTGTGCTTCAACGCGAATTCAGAGCTTTGATCTCACTCACTAAACCAACGAGCT 906
Db 618 TCAGTTGTGCTTCAACGCGAATTCAGAGCTTTGATCTCACTCACTAAACCAACGAGCT 677
Qy 907 GCTTTTCACTCTTGGAACTTCTTGTATTTTCTTCTTAACTGACCTTGGTGGTCT 966
Db 678 GCTTTTCACTCTTGGAACTTCTTGTATTTTCTTCTTAACTGACCTTGGTGGTCT 737
Qy 967 GCAACCGCTGTGATAAGTGCCTGATCTTATCAAGAGCTATATCTTGGAGGCACTCAACT 1026
Db 738 GCAACCGCTGTGATAAGTGCCTGATCTTATCAAGAGCTATATCTTGGAGGCACTCAACT 797
Qy 1027 GACGAGAGTTGCCCTTATGATCTTATGCGTATCTTTCTTATATGCTTGGTGGTCT 1086
Db 798 GACGAGAGTTGCCCTTATGATCTTATGCGTATCTTTCTTATATGCTTGGTGGTCT 857
Qy 1087 TCGACTTGGGGTATCTCTCACTGTTTCTGCTGTTATGCTGATGCTCCCATTTACACA 1146
Db 858 TCGACTTGGGGTATCTCTCACTGTTTCTGCTGTTATGCTGATGCTTCACTTACTCC 917
Qy 1147 TGGCAATGTAAACGAGAGCTCAAGATAACAAACAAAGATACCTTTGCAACTTTGTCA 1206
Db 918 TGGCATCAAGTGACAGAGAGATTTAAGTTACCAACAGCATTCATTTGTAACTTTAGGA 977
Qy 1207 TTTCTGCGGAGACATTTATTTTCTTGTATGTTGGAATGGATGCTTGGACATTCGACAG 1266
Db 978 TTTCAATTCGAACATTTCTCTGCTCTATGTTAAACATGGATATATTGGACCTAGAGGAC 1037
Qy 1267 TGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCAGTGAGCTCAATCCTAATGGGT 1326
Db 1038 TGGAGATTTAGCTAGTCTAGAGTCTTAAAGAGACCAATTTCTGTTAACTGCAATTTATTTGACA 1097
Qy 1327 CTGCTCATGTTTGAAGAGCAGCGTTTCTCTTTCCGTTATCGTTTCTTCTATCAACTTAGCC 1386
Db 1098 TTGGTTATGATTTGNAAGAGTCGATTTATATTCCTTTTGAATTTGCGATCCACCTACNA 1157
Qy 1387 AAGAAGAAATCAACGCGAGAAAATCAACTTTTAAACATGCGAGGTTGTGATTTGGTGGTCT 1446
Db 1158 AAAGGGGACGCGGATCCCAAGAAATCAACTTCGAAAACACAACCTAATCTTATGGTTCGCTAGT 1217
Qy 1447 CTCATGAGAGTGTGTTATCTATGGCTTTCATACACAAAGTTTACAAAGGCGCGGCAC 1506
Db 1218 CTCATGAGAGGACAAATTTTCAAGTTTCGCGTCTTTTATACCAAGTTTAAACGCACTGGTCCAC 1277
Qy 1507 ACAGATGTACCGGGAATGCAATCATGATCAGAGTACGATAAATGCTGCTCTTTTATAGC 1566
Db 1278 TCTGAATCCGACTCAATGTCTATGATTAACAGCACATTTATTTGTTATTTCTATTCGGC 1337
Qy 1567 ACAGTGGTGTGTTGGTATGCTGACCAAAACCACTATAAGCTACCTATTAACCGC 1618

Db 1338 ACAATGGCTTTCAACCTGGTGACGCGCCGGTAGCAAGTATCTCTCCACC 1389

RESULT 14
AAA72926
ID AAA72926 standard; DNA; 1668 BP.
XX
AC AAA72926;
XX
XX 06-AUG-2003 (revised)
DT 23-NOV-2000 (first entry)
XX
XX Atliplex gmelini Na⁺ and H⁺ antiporter protein encoding DNA.
XX
XX Atliplex gmelini; Na plus and H plus antiporter protein;
KW Na⁺ and H⁺ antiporter protein; transformed plant; high salt tolerance;
KW ds.
XX
XX Atriplex gmelini.
XX
PN JP2000157287-A.
XX
PD 13-JUN-2000.
XX
PF 16-SEP-1999; 99JP-00261606.
XX
PR 24-SEP-1998; 98JP-00269504.
XX
PA (SHOK-) SHOKUBUTSU KOGAKU KK.
XX
XX WPI; 2000-468209/41.
DR P-PSDB; AAB12786.
XX
XX An Na⁺ and H⁺ plus antiporter protein and a gene encoding it.
PT
PS Claim 1; Page 9-10; 16pp; Japanese.
XX
XX The present sequence encodes an Na⁺ and H⁺ antiporter protein isolated
CC from Atriplex gmelini. The Na⁺ and H⁺ antiporter protein and gene
CC encoding it are useful for the preparation of transformed plants with
CC high salt tolerance, e.g. for growth in arid land. (Updated on 06-AUG-
XX 2003 to correct OS field.)
SQ Sequence 1668 BP; 397 A; 342 C; 376 G; 553 T; 0 U; 0 Other;

Query Match 38.2%; Score 832.8; DB 3; Length 1668;
Best Local Similarity 71.9%; Pred. No. 4.5e-178;
Matches 1146; Conservative 0; Mismatches 412; Indels 36; Gaps 3;

QY 323 CGACATCTGATCACGCTTCTGGTGGTGGTGAATCTCTTTGTCACCTCTTTGGTGT 382
DB 50 CCACCTCTGATCACGCTTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 109

QY 383 GTATTGTTCTTGGTCTATCTTTTGAAGAGAAATAGATGGATGAACCAATCCATCACGCGCT 442
DB 110 GTATCGTAATTTGGTCTATCTCTAGAGGAGATCGTTGGATGAATGAGTCCATCTGCGCC 169

QY 443 TTTGATTGGGTAGGCACTGGTGTACCATTTTGTGATTAGTAAAGAAAAGCTGCG 502
DB 170 TTTCTATAGGTTTGGCTACTGGGGTGTGATTTCTGCTGATTAGTGGAGGAAAAGTTTCA 229

QY 503 ATCTTCTCTGTTAGTGAAGATCTTTTCTCATATATCTTTTGGCCACCCATATATTTCA 562
DB 230 ATCTTTTGGTCTCTAGTGAAGATCTTTTCTCATATATCTTTTCCACCGATTATTTCA 289

QY 563 ATGCAAGGTTTCAAGTAAAGAAAGACAGTTTTCGCAATTTCTGTGACTATTATGCTTT 622
DB 290 ATGCAAGGTTTCAAGTGAAGAGAGAGAGTCTTCCGCACTTCAATTACTATTGATTGT 349

QY 623 TTGGTGTCTTGGGACTATATTATTTCTTGCACAATCATATCTCTAGGTGTAAACAGTTCT 682
DB 350 TTGGAGCTGTGGTACATTTGGTATCATTTCACTCACCATCATATCTCTGGGAGGCTTGTCAAATTT 409

QY 683 TTAAGAAAGTTGGACATTTGGAACCTTTGACTTGGGTGATATCTTTGCTATTGCTGTCATAT 742
DB 410 TTAAGAAAGTTGGATATTTGGTACTCTCTGGAGTTGGCAGACTATCTTGCATTTGGTGAATAT 469

QY 743 TTGCTGCAACAGATTTCAGTATGTACACTGCAAGGTTTCTGAATCAAGACGAGACACTTTGCG 802
DB 470 TCGCTGCCACAGATTCTGTTTGGCAGACTGCACTGCAAGGTTCTTAATACAGATGAGACCCCTCTGC 529

QY 803 TTTACAGTCTTTGATTCGGAGAGGGTGTGTGAATGATGCAACCTGCTAGTTGTGCTTTCA 862
DB 530 TCTACAGTCTGGTCTTTGGCGAGGGTGTGTGAATGATGCAACCTGCTAGTTGTGCTTTCA 589

QY 863 ACGGATTCAGAGCTTTGATCTCACTCACCTAAACACGAGCTGCTTTTCATCTCTTTG 922
DB 590 ATGCAATTCAGAGCTTTGACCTCAAGAAATTTGATCACAGATAGCTTTTCAATTTATGG 649

QY 923 GAAACTCTCTGTTATTTGTTCTCCTAAAGTACTCTTGGTGGTGGTGGTGGTGGTGGTGGT 982
DB 650 GCAACTCTCTTATATTTTATTCGCAAGCAGTACTTTGGAGCAATTTACTTGGCTTGCTCA 709

QY 983 GTGCTATGTTATCAAGAGCTATACCTTTGGAAGGCACTCAACTGACGAGAGGTTGCCC 1042
DB 710 GTGCTTACATTTATCAAAAAGCTGTACTTTGGAAGGCAATTTCCACTGATCGTGGAGTTGCTT 769

QY 1043 TTATGATGCTTATGCGGTATCTTTCTTATATGCTTGTGCTGCTTTTCGACTTTGAGCGGTA 1102
DB 770 TAATGATGCTTATGCGCTTATCTTATCTTACATGCTTGTGCTGAACCTTTCTATTGAGTGGAA 829

QY 1103 TCCTCAGTGTGTTTTTCTGTGGTATTTGTGATGTCCCATTTACATATGGCACAATGTAACGG 1162
DB 830 TTTCTTACTGTATTTCTTCTGTGGGATTTGTCAATGCCATTTATCTTGGCACAATGTGACAG 889

QY 1163 AGAGCTCAAGATTAACAACAAAGCATACCTTTGCAACTTTGCTCATTTCTTCCGAGACAT 1222
DB 890 AGAGCTCAAGAGTAAACCAAGCATGCTTTTGAACATATCTTTTGTGCTGAGGTTT 949

QY 1223 TTATTTTCTGTTATGTTGGAATGATGCTTTGGACATTTGCAAGTGGAGATTCCTGTAGTG 1282
DB 950 TCCTATTCTTATATGTCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1009

QY 1283 ACACACCGGGAACATCGATCGAGTCAATCTTAATGGGTCTGGTCAATGTTGGAA 1342
DB 1010 ATAGTCTCTGGCATTTCTGTTGCTGAGTTCCATATTTGCTAGGTCTAGTCAATGTTGGAA 1069

QY 1343 GAGCAGGTTGCTTCTTCCGTTATCGTTTCTATCTAATCTTAGCCAAAGATCAAAAGCG 1402
DB 1070 GAGCAGCTTTTGTGTTTCCCTTATCTCTGGTGTGATGAACTTTGCCAAGAAATCGCAAGTG 1129

QY 1403 AGAAAATCAACTTTTAAATGCAAGTGTGATTTGGTGTCTGGTCTCATGAGAGTGTGCTG 1462
DB 1130 AAAAGGTCACTTTTCAACAGCAGATTTGTATGTTGGGTGGTGGTGGTGGTGGTGGTGGTGG 1189

QY 1463 TATCTATGGCTTTTGCATACAACAAAGTTTACAAGGCGCGGCAACACAGATGTACGCGGA 1522
DB 1190 TTTCCATGGCACTTTTATATTAATCAGTTTACAGGTTCTGGGCAACACAGCTTAGGGGAA 1249

QY 1523 ATGCAATCATGATCAGAGTACGATACTGTCTCTTTTGTAGCAGTGTGTTGGTA 1582
DB 1250 ATGCAATCATGATCACAAGCACTATATCTGTTGCTCTTTTGTAGTACATGTTGTTGGGT 1309

QY 1583 TGCTGACCAACCACTCATAGCTTACCTATTTACCGCACCAAGCCGCAACAC-----GA 1636
DB 1310 TGCTGACCAAGCTCTCATATGTTTGTGCTCTAACCGAACAATTTCACTAGTTGCA 1369

QY 1637 GCATGTTTATCTGATGACAACCCCAAAAT-----CC 1668
DB 1370 GCACCGTATCAGATGTGGGAAGTCCAAAGTCATACTCGTTGCCACTCTTGGGCGCAACC 1429

QY 1669 ATACATATCCCTTTTGGACCAAGACTCGTTGTTGAGCTTTCAGGGAACAC--AATG 1726
DB 1430 AAGATTATGAAGTTGATGTGGGAAACCGAAACCACTAAGACACCACTGAGCCGGGACTA 1489

QY 1727 TGCCTCGGCTTGACAGTATACGTGGCTTCTTGACACGCGCCCACTCGAACCCTGCACTACT 1786

```

Db      1490  TAGTTGACCTAGTAGCCTCCGCATGCTTTCTAAATGCACTACTCAACCGTCCATCACT 1549
QY      1787  ACTGGAGACAATTTGATGACTCTTTCATGCGACCGCTTTTGGAGTCTGGCTTTGTAC 1846
Db      1550  ATTGGCGCAATTCGATGACTCTTTCATGCGGCCCTTTTGGTGGCCGGGTTTGTAC 1609
QY      1847  CTTTGTTCAGGTTCTCAACTGAGAGAAACC 1880
Db      1610  CTTTGTCCGGTTTCACTACTGAAACAAAGCAC 1643

RESULT 15
AAF75765
ID      AAF75765 standard; DNA; 2553 BP.
XX
AC      AAF75765;
XX
DT      14-MAY-2001 (first entry)
XX
DE      Gene regulating the pH of vacuoles.
XX
KW      Vacuole pH regulation; flower colour; ds.
XX
OS      Nierembergia hybrida.
XX
PN      WO200114560-A1.
XX
PD      01-MAR-2001.
XX
PF      24-AUG-2000; 2000WO-JP005722.
XX
PR      24-AUG-1999; . 99JP-00236800.
XX
PA      (SUNR ) SUNTORY LTD.
XX
PI      Iida S, Tanaka S, Inagaki Y;
XX
DR      WPI; 2001-191648/19.
XX
P-PSDB; AAB73253.
XX
PT      Morning glory-originated gene encoding a protein with pH regulation
PT      activity in vacuoles, useful in controlling flower color to give new
PT      breeds of colorful plants for cut flowers, particularly applicable in
PT      horticulture.
XX
PS      Example 7; Page 45-49; 68pp; Japanese.
XX
CC      The present sequence is a gene, which encodes a protein with vacuolar pH
CC      regulatory activities. The gene enables flower colour to be controlled
CC      via regulation of the vacuolar pH, colours can range from blue to red in
CC      colour spectrum. The gene is useful in controlling flower colour to give
CC      new breeds of colourful plants for cut flowers, particularly applicable
CC      in horticulture
XX
SQ      Sequence 2553 BP; 666 A; 487 C; 535 G; 865 T; 0 U; 0 Other;

Query Match      37.7%; Score 821.2; DB 4; Length 2553;
Best Local Similarity 70.3%; Pred. No. 2.1e-175;
Matches 1115; Conservative 0; Mismatches 468; Indels 3; Gaps 1;

QY      289  TTGATCTCTAGTGCAGAACTGCCTTCTGTTATCGACATCTGATCAGCTTCTGTGTT 348
Db      543  TTTGGGACTCTGCTGGGAAGATGAACAACCTTCAACTCTGATCAATCAATCAGTGGTG 602
QY      349  GCGTTGAATCTCTTTGTGCACTCTTTGTGCTGTGTTATGTTCTTTGGTCATCTTTTGGAA 408
Db      603  TCGGTAACCTCTTTGTTGCACTTATTTGCGCGTGTATTTGTGATCGGTCATTTATGGAG 662
QY      409  GAGAATAGATGATGAACGAATCCATCCCGCTTGTGTTGATTTGGGCTAGGCACTGGTGT 468
Db      663  GAAAAACAGATGATGAATGAGTCCATAACTGCGCCTTGTGATGTTGATGTCAGTGGAGTC 722

```

```

QY      469  ACCATTTTGTGATTAAGTAAAGAAAAAGCTCGCATCTTCTCGTCTTTAGTAGAAGATCTT 528
Db      723  ATCAATCTACTAATAAGTGGAGGAAAGAACTCACATAATTTTAGTGTTCAGCGAAGATCTT 782
QY      529  TTCCTCATATATCTTTTGGCCACCCCAATATATTCATATGACAGGTTTCAAGTAAAAAAGAG 588
Db      783  TTCCTCATATTAACCTTCTTCCACCGCATCAATTTTAAATGCTGGGTTCCAGGTGAAAAAGAA 842
QY      589  CAGTTTTTCCGCAATTTTCTGACTATATGCTTTTGGTGTGCTTTGGGACTATATTTCT 648
Db      843  TCATTTCTCCGCAATTTTCACTATCATGCTTTTGGGAGTGGGACCTTGATATCG 902
QY      649  TGCACAATCATATCTTAGGTGAACACAGTTTCTTTAAGAAAGTTGGACATTCGAACTTTT 708
Db      903  TTCAATTAATATACAGCGGTGCTATTGGCAATTTTCAAGAAATGGATATTGGACACCTT 962
QY      709  GACTTGGGTGATATCTTGTCTATTTGGTGCCATATTTGCTGCAACAGATTCAGTATGTACA 768
Db      963  GAAATTGGAGATTACCTTGGCAATTGGAGCAATCTTTGCTGCAACAGATTCGTATGCACC 1022
QY      769  CTGCAGGTTTCTGAATCAAGACGAGACACCTTTGCTTTTACAGTCTTGTATTCGAGAGGCT 828
Db      1023  TTACAAGTCTTAATCAGAAAGAAACCGTTATTGTACAGTCTAGTGTTTGGAGAAGT 1082
QY      829  GTTGTGAATGATCAACCGTCACTGTTGTGCTTCAACGCGATTCAGAGCTTTTGTATCTCACT 888
Db      1083  GTTGTGAATGATGCCACATCTGTAGTGTCTTCAATGCTGTCCAGAACTTTGACTTATCT 1142
QY      889  CACCTAAACACGAGAGCTGCTTTTCACTTTTGGAAACTTCTTGTATTTGTTTCTCTTA 948
Db      1143  CATATCAGCAGCAGGCAAAAGCTCTGCAATTAATTTGAAAACCTTTCTATATCTTGTTCCTCG 1202
QY      949  AGTACTTGTCTGGTCTGCAACCGTCTGATAGTGGTATGTTATCAAGAGATATAC 1008
Db      1203  AGCACTTCTTAGGGGTTGCTGTGGCCTACTAAGTGCCTTTATTAATTAAGAAACTCTAC 1262
QY      1009  TTTGGAAGGCACTCAACTGACCGAGAGGTTGCGCTTATGATGCTTATGGCGTATCTTTCT 1068
Db      1263  TTTGGAAGGCACTCGACTGATCGTGAGTTGCTATAATGATACTCATGCGGTACCTATCA 1322
QY      1069  TATATGCTTGTGAGCTTTTTCGACTTTGAGCGGTATCTCACTGTGTTTCTGTGGTATT 1128
Db      1323  TACATGCTTGTGGAATTAATTTCTTAAAGTGAATCTCTCACTGTGTTTCTGTGGGATC 1382
QY      1129  GTGATGTCCTCATACATGTCACAACTGTAACGAGAGCTCAAGATTAACACAAAGAT 1188
Db      1383  GTGATGTCCTCATATACCTGGCATAATGTGACTGAGAGCTCAAGAGTCACTACCAGGAC 1442
QY      1189  ACCTTTGCACCTTTTGTCAATTTCTTGGGAGACATTTATTTCTGTATGTTGGAAATGGAT 1248
Db      1443  ACGTTTGTACATATCAATTTATTTGCTGAATATTCATATTCCTTTATGTTGGTATGAT 1502
QY      1249  GCCTTGGACATGACAAAGTGGAGATCCGTGAGTGACACACCGGGAAACATCGATCCAGTG 1308
Db      1503  GCTTTGGACATGGAAGTGAAGTTTGTAAAGCGACAGCCCCCGGAACATCAATTAAGGTC 1562
QY      1309  AGCTCAATCTTAATGGGTCTGTCATGTTTGGAGAGCAGGTTGCTTTTCCGTATATCG 1368
Db      1563  AGCTCAATTTGCTAGGTCTTGTGTTTGGAGGGGAGGCTTTGTTTCTCCCTTTGTCA 1622
QY      1369  TTTCTATCTAACTTAGCCCAAGAAGAAATCAAAAGCGAGAAATCAACTTTAAATGACAGGTT 1428
Db      1623  TTCTTGTCAACTTGACCCAGAAAATCTCAGGACAAGATTAGCTTTAACGACAGGTT 1682
QY      1429  GTGATTTGGTCTGGTCTCATGAGAGGTCTGTATCTATGGCTCTTTGGCATACAAAG 1488
Db      1683  ACAATATGTTGGCTGGGCTTATGCGAGGTCTGTCTTCTATGGCCCTTCTGTTATAATCAG 1742
QY      1489  TTTACAGGGCCGGGCACACAGATGTAGCGGGAAATGCAATCATGATCAGAGTACGATA 1548
Db      1743  TTTACAGGGGAGGTCATCTCAGTTACGTGCCAATGCAATGAATGATCAGAGTACTATC 1802
QY      1549  ACTGTCCTCTTTTGTAGCACAGTGTGTTTGTGTTATGCTGACCAAAACC---ACTCATAGC 1605

```

[illegible]

Search completed: August 28, 2005, 02:57:21
Job time : 1191 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 28, 2005, 05:36:26 ; Search time 1432 Seconds
(without alignments)
9951.711 Million cell updates/sec

Title: US-10-617-624-1
Perfect score: 2178
Sequence: 1 cctctctgttccttcctcg.....aaaaaaaaaaaaaaaaaaaaa 2178

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7331713 seqs, 327154945 residues
Total number of hits satisfying chosen parameters: 14663426

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

1:	/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2:	/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
3:	/cgn2_6/ptodata/2/pubpna/US05_PUBCOMB.seq:*
4:	/cgn2_6/ptodata/2/pubpna/US04_PUBCOMB.seq:*
5:	/cgn2_6/ptodata/2/pubpna/US03_PUBCOMB.seq:*
6:	/cgn2_6/ptodata/2/pubpna/US02_PUBCOMB.seq:*
7:	/cgn2_6/ptodata/2/pubpna/US01_PUBCOMB.seq:*
8:	/cgn2_6/ptodata/2/pubpna/US00_PUBCOMB.seq:*
9:	/cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10:	/cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11:	/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12:	/cgn2_6/ptodata/2/pubpna/US09D_PUBCOMB.seq:*
13:	/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14:	/cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15:	/cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16:	/cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17:	/cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18:	/cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19:	/cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
20:	/cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
21:	/cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
22:	/cgn2_6/ptodata/2/pubpna/US10J_PUBCOMB.seq:*
23:	/cgn2_6/ptodata/2/pubpna/US10K_PUBCOMB.seq:*
24:	/cgn2_6/ptodata/2/pubpna/US10L_PUBCOMB.seq:*
25:	/cgn2_6/ptodata/2/pubpna/US10M_PUBCOMB.seq:*
26:	/cgn2_6/ptodata/2/pubpna/US10N_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2178	100.0	2178	21	US-10-617-624-1
2	2178	100.0	2178	21	US-10-617-624-1
3	1617	74.2	1617	9	US-09-938-842A-1239
4	1617	74.2	1617	11	US-09-938-842A-1239
5	1149.4	52.8	2136	14	US-10-155-535-1
6	1149.4	52.8	2136	24	US-11-067-456-1
7	1149.4	52.8	2136	24	US-11-067-558-1

8	837.4	38.4	1915	18	US-10-425-114-20609
9	821.8	37.7	1968	18	US-10-424-599-58707
10	797.6	36.6	1620	17	US-10-369-324-38
11	797.6	36.6	1620	19	US-10-607-538-38
12	794.4	36.5	1621	17	US-10-369-324-37
13	794.4	36.5	1621	19	US-10-607-538-37
14	768.8	35.3	2330	21	US-10-944-174-1
15	719	33.0	2066	14	US-10-155-535-3
16	719	33.0	2066	24	US-11-067-456-3
17	719	33.0	2066	24	US-11-067-558-3
18	682.6	31.3	1638	17	US-10-409-701-22
19	682.6	31.3	2222	20	US-10-425-115-153633
20	655.2	30.1	2131	20	US-10-739-930-4043
21	553	25.4	1719	20	US-10-425-115-90586
22	546.2	25.1	1669	19	US-10-437-963-92579
23	521.4	23.9	1841	20	US-10-425-115-11149
24	468.2	21.5	1014	18	US-10-425-114-21998
25	418	19.2	418	9	US-09-770-423-408
26	415.2	19.1	1896	19	US-10-437-963-46695
27	291.4	13.4	805	18	US-10-425-114-30183
28	269.2	12.4	612	19	US-10-021-323-8200
29	239	11.0	420	19	US-10-767-701-18258
30	165.4	7.6	601	19	US-10-767-701-2295
31	165.2	7.6	466	11	US-09-732-627A-3880
32	165.2	7.6	466	19	US-10-767-795-2863
33	163.4	7.5	1159	20	US-10-425-115-11150
34	161.2	7.4	515	19	US-10-767-701-22357
35	152.2	7.0	573	19	US-10-021-323-2361
36	149.4	6.9	596	19	US-10-021-323-15135
37	146.4	6.7	437	20	US-10-425-115-129116
38	146.4	6.7	2000	9	US-09-938-842A-3933
39	146.4	6.7	2000	11	US-09-938-842A-3933
40	141.8	6.5	1824	10	US-09-991-936-1870
41	141.8	6.5	1824	10	US-09-991-936-1871
42	141.8	6.5	2080	10	US-09-991-936-1867
43	141.8	6.5	2080	10	US-09-991-936-1869
44	139.8	6.4	859	19	US-10-767-701-7658
45	135	6.2	853	20	US-10-425-115-156434

ALIGNMENTS

RESULT 1
US-10-617-623-1
; Sequence 1, Application US/10617623
; Publication No. US2005002823SAI
; GENERAL INFORMATION:
; APPLICANT: Zhang, Hong-Xia
; APPLICANT: Blumwald, Eduardo
; TITLE OF INVENTION: PLANT FRUIT WITH ELEVATED POTASSIUM
; TITLE OF INVENTION: LEVELS
; FILE REFERENCE: 529642000300
; CURRENT APPLICATION NUMBER: US/10/617.623
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: US 60/395,637
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2178
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-617-623-1

Query Match 100.0%; Score 2178; DB 21; Length 2178;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCTCTCTGTTTCGTTCTCTCGTAGCAGAGAGAGAGAAATCTCAGTTTAGCTTTCGA 60
Db 1 CCTCTCTGTTTCGTTCTCTCGTAGCAGAGAGAGAGAAATCTCAGTTTAGCTTTCGA 60

QY 61 AGCTTCCAAATTTTGAATTTTGTATCTCTGGGCTCTTTTGTAAATCAGACTGAAGATAT 120
Db |||||
QY 61 AGCTTCCAAATTTTGAATTTTGTATCTCTGGGCTCTTTTGTAAATCAGACTGAAGATAT 120
Db |||||
QY 121 TTAGATTACCCAGAAAGTTGTTCAAGGAATGTTTTCAGTGGACAGCA CGGAAGAGATAAAG 180
Db |||||
QY 121 TTAGATTACCCAGAAAGTTGTTCAAGGAATGTTTTCAGTGGACAGCA CGGAAGAGATAAAG 180
Db |||||
QY 181 AGACTTTTTCAGAGATTTTGTCTGATCGAATCTGAATAGTTTCAATGTTCTTGGAT 240
Db |||||
QY 181 AGACTTTTTCAGAGATTTTGTCTGATCGAATCTGAATAGTTTCAATGTTCTTGGAT 240
Db |||||
QY 241 CAATCTCGAAGAGAAAGTTTGTGGATCTAGAAAGAGATAAATGTTGGATTTCTCTA 300
Db |||||
QY 301 GTGTGCGAAATCGCTTCGTTATTCGACATCTGATCAACGCTTCTGTGGTTGCGTTGAATCTC 360
Db |||||
QY 301 GTGTGCGAAATCGCTTCGTTATTCGACATCTGATCAACGCTTCTGTGGTTGCGTTGAATCTC 360
Db |||||
QY 361 TTGTGTCACATCTTTGTGCTGTTATGTTCTGTGTCATCTTTTGGAAAGAGATAGATGG 420
Db |||||
QY 361 TTGTGTCACATCTTTGTGCTGTTATGTTCTGTGTCATCTTTTGGAAAGAGATAGATGG 420
Db |||||
QY 421 ATGAACGAATCCATCAACCGCTTGTGATTTGGCTAGGACCTGCTGTTACCATTTTGTG 480
Db |||||
QY 421 ATGAACGAATCCATCAACCGCTTGTGATTTGGCTAGGACCTGCTGTTACCATTTTGTG 480
Db |||||
QY 481 ATTAGTAAGGAAAGCTCGCATCTTCTCGTCTTTAGTGAAGATCTTTTCTTCATATAT 540
Db |||||
QY 481 ATTAGTAAGGAAAGCTCGCATCTTCTCGTCTTTAGTGAAGATCTTTTCTTCATATAT 540
Db |||||
QY 541 CTTTGTGCAACCATTAATTAATCGACGGTTTCAAGTAAAGAGAGAGATTTTTCGC 600
Db |||||
QY 541 CTTTGTGCAACCATTAATTAATCGACGGTTTCAAGTAAAGAGAGAGATTTTTCGC 600
Db |||||
QY 601 AATTTTCGTGACTATTAATGCTTTTCTGCTGTTGGACTATTAATTTCTTGACAAATCATA 660
Db |||||
QY 601 AATTTTCGTGACTATTAATGCTTTTCTGCTGTTGGACTATTAATTTCTTGACAAATCATA 660
Db |||||
QY 661 TCTCTAGGTGTAACAGTTCTTTAAGAGTTGACATTTGGAACCTTTGACTTTGGGTGAT 720
Db |||||
QY 661 TCTCTAGGTGTAACAGTTCTTTAAGAGTTGGAATTTGGAACCTTTGACTTTGGGTGAT 720
Db |||||
QY 721 TATCTTGCTATTTGGTGCCATATTTGCTGCAACAGATTCAGTATGTACACTGCGAGTTCTG 780
Db |||||
QY 721 TATCTTGCTATTTGGTGCCATATTTGCTGCAACAGATTCAGTATGTACACTGCGAGTTCTG 780
Db |||||
QY 781 AATCAAGACGACACCTTTGCTTTTACAGTCTTGTATTCGGAGAGGGTGTGTGAATGAT 840
Db |||||
QY 781 AATCAAGACGACACCTTTGCTTTTACAGTCTTGTATTCGGAGAGGGTGTGTGAATGAT 840
Db |||||
QY 841 GCAAGCTCAGTTGTTGCTTCAACCGGATTCAGAGCTTTGATCTCACTCACTCAACCCAC 900
Db |||||
QY 841 GCAAGCTCAGTTGTTGCTTCAACCGGATTCAGAGCTTTGATCTCACTCACTCAACCCAC 900
Db |||||
QY 901 GAAGCTGCTTTTCACTCTTTGGAACCTTTGTTATTTGTTCTCCTAAGTACCTTGCTT 960
Db |||||
QY 901 GAAGCTGCTTTTCACTCTTTGGAACCTTTGTTATTTGTTCTCCTAAGTACCTTGCTT 960
Db |||||
QY 961 GGTGCTGCAACCGGTCGATAGTGGTATGTTATCAAGAGCTATATCTTTTGGAGGAC 1020
Db |||||
QY 961 GGTGCTGCAACCGGTCGATAGTGGTATGTTATCAAGAGCTATATCTTTTGGAGGAC 1020
Db |||||
QY 1021 TCAACTGACCGAGAGTTGCCCTTATGATGCTTATGGGTATCTTTCTTATATGCTTGTCT 1080
Db |||||
QY 1021 TCAACTGACCGAGAGTTGCCCTTATGATGCTTATGGGTATCTTTCTTATATGCTTGTCT 1080
Db |||||
QY 1081 GAGCTTTTCGACTTGAGCGGTATCCCTGCTGTTTCTGTTGTTTCTGTTGTTTCTGATGCCAT 1140
Db |||||
QY 1081 GAGCTTTTCGACTTGAGCGGTATCCCTGCTGTTTCTGTTGTTTCTGTTGTTTCTGATGCCAT 1140
Db |||||
QY 1141 TACACATGGCAATGTAAACGGAGAGCTCAAGAAATAACAAACAGCATACCTTTTGCAACT 1200

Db ||||| TACACATGGCAATGTAAACGGAGAGCTCAAGAAATAACAAACAGCATACCTTTTGCAACT 1200
QY 1201 TTGTCAATTTCTTGGAGAGACATTTATTTCTTGTATGTTGGAAATGGAATGCTTGGACATTT 1260
Db |||||
QY 1201 TTGTCAATTTCTTGGAGAGACATTTATTTCTTGTATGTTGGAAATGGAATGCTTGGACATTT 1260
Db |||||
QY 1261 GACAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGAGTGAGCTCAATCCTA 1320
Db |||||
QY 1261 GACAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGAGTGAGCTCAATCCTA 1320
Db |||||
QY 1321 ATGGCTCTGGTCAATGTTTGAAGAGCAGCGTTCTGTTTTCGTTATCGTTTCTATCTAAC 1380
Db |||||
QY 1321 ATGGCTCTGGTCAATGTTTGAAGAGCAGCGTTCTGTTTTCGTTATCGTTTCTATCTAAC 1380
Db |||||
QY 1381 TTAGCCAAAGAAATCAAGCGAGAAATCAATTTTAAACATGCAAGTTTGAATTTGGTGG 1440
Db |||||
QY 1381 TTAGCCAAAGAAATCAAGCGAGAAATCAATTTTAAACATGCAAGTTTGAATTTGGTGG 1440
Db |||||
QY 1441 TCTGCTCTCATGAGAGGTGCTGTATCTATGGCTCTTGCATACAAAGTTTGAAGGCCC 1500
Db |||||
QY 1441 TCTGCTCTCATGAGAGGTGCTGTATCTATGGCTCTTGCATACAAAGTTTGAAGGCCC 1500
Db |||||
QY 1501 GGGCACACAGATGTACCGGGAATGCAATCATGATCAGAGTACGATAAATGCTGCTCTT 1560
Db |||||
QY 1501 GGGCACACAGATGTACCGGGAATGCAATCATGATCAGAGTACGATAAATGCTGCTCTT 1560
Db |||||
QY 1561 TTTAGCACAGTGTGTTGTTGATGCTGACCAACCACTATTAAGCTACTATTAACCGCAC 1620
Db |||||
QY 1561 TTTAGCACAGTGTGTTGTTGATGCTGACCAACCACTATTAAGCTACTATTAACCGCAC 1620
Db |||||
QY 1621 CAGAACCCACACGAGCATGTTATCTGATGACAAACCCCAAAATCCATACATATCCCT 1680
Db |||||
QY 1621 CAGAACCCACACGAGCATGTTATCTGATGACAAACCCCAAAATCCATACATATCCCT 1680
Db |||||
QY 1681 TTGTGGAACCAAGACTCGTTTCAATGAGCTTTCAGGGAACCAAAATGTCCTCGGCTGAC 1740
Db |||||
QY 1681 TTGTGGAACCAAGACTCGTTTCAATGAGCTTTCAGGGAACCAAAATGTCCTCGGCTGAC 1740
Db |||||
QY 1741 AGTATAGCTGGCTTTCTTGACACCGCCCACTCGAACCCGTCATTAATCTGAGAGACAATTT 1800
Db |||||
QY 1741 AGTATAGCTGGCTTTCTTGACACCGCCCACTCGAACCCGTCATTAATCTGAGAGACAATTT 1800
Db |||||
QY 1801 GATGACTCTTCATGCGACCGCTCTTTGGAGGCTGCTGCTTGTACCCCTTTGTTCCAGGT 1860
Db |||||
QY 1801 GATGACTCTTCATGCGACCGCTCTTTGGAGGCTGCTGCTTGTACCCCTTTGTTCCAGGT 1860
Db |||||
QY 1861 TCTCCAACTGAGAGAAACCTCTCTGATCTTAGTAAGCTTGAAGGTAAACGTTGGAAGAAA 1920
Db |||||
QY 1861 TCTCCAACTGAGAGAAACCTCTCTGATCTTAGTAAGGCTTGAAGGTAAACGTTGGAAGAAA 1920
Db |||||
QY 1921 GCTTTGATTTTGTGTAAGAAAGGTTGATTCAAATTAATGCTTTGTGTAATATTCCTA 1980
Db |||||
QY 1921 GCTTTGATTTTGTGTAAGAAAGGTTGATTCAAATTAATGCTTTGTGTAATATTCCTA 1980
Db |||||
QY 1981 TTTGTAATATTTGTTGTAAGAGACAAATCTGCTCAACCGTTTGAAGAGAGGACAA 2040
Db |||||
QY 1981 TTTGTAATATTTGTTGTAAGAGACAAATCTGCTCAACCGTTTGAAGAGAGGACAA 2040
Db |||||
QY 2041 ACATGGCAACTTTTGAAGTGTGTTGATGATGTAATTAATTAATTAATTTGTTGTTG 2100
Db |||||
QY 2041 ACATGGCAACTTTGAGAGTGTGTTGATGATGTAATTAATTAATTAATTTGTTGTTG 2100
Db |||||
QY 2101 TAAACAAACTACATTTGTTTGAATTTGTTGTTTCTGCTCGAAAAAATAA 2160
Db |||||
QY 2101 TAAACAAACTACATTTGTTTGAATTTGTTGTTTCTGCTCGAAAAAATAA 2160
Db |||||
QY 2161 AAAAAAATAAATAAATAA 2178
Db |||||
QY 2161 AAAAAAATAAATAAATAA 2178
Db |||||

RESULT 2

Db 1321 TACCTATTACCGCACCAAGACGCCACACGAGCATGTATCTGATGACCAACCCCAAAA 1380
QY 1666 TCCATACATATCCCTTTGTTGGACCAAGACTCGTTCANTGAGCCTTCAGGGAACCACAAT 1725
Db 1381 TCCATACATATCCCTTTGTTGGACCAAGACTCGTTCANTGAGCCTTCAGGGAACCACAAT 1440
QY 1726 GTGCTCGGCTGACAGTATACGTGGCTTTGACACGGCCCACTCGAACCGTGCATTAC 1785
Db 1441 GTGCTCGGCTGACAGTATACGTGGCTTTGACACGGCCCACTCGAACCGTGCATTAC 1500
QY 1786 TACTGGAGACAAATTGATGACTCCTTCATGCGACCCGCTCTTTGAGAGTCTGGCTTTGTA 1845
Db 1501 TACTGGAGACAAATTGATGACTCCTTCATGCGACCCGCTCTTTGAGAGTCTGGCTTTGTA 1560
QY 1846 CCCTTTGTTCCAGGTTCTCCAACTGAGAGAAAACCTCCTGATCTTATAGTAAGGCTTGA 1902
Db 1561 CCCTTTGTTCCAGGTTCTCCAACTGAGAGAAAACCTCCTGATCTTATAGTAAGGCTTGA 1617

RESULT 4

US-09-938-842A-1239
; Sequence 1239, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1239
; LENGTH: 1617
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1239

Query Match 74.2%; Score 1617; DB 11; Length 1617;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1617; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 286 ATGTTGGATTCTCTAGTGTGCAAACTGCCCTTCGTTATCGACATCTGATCAACGCTTCTGTG 345
Db 1 ATGTTGGATTCTCTAGTGTGCAAACTGCCCTTCGTTATCGACATCTGATCAACGCTTCTGTG 60
QY 346 GTTGGCTTGAATCTCTTTGTTGACATCTTTGCTGTTGATTTGTTCTTGGTCACTTTTGG 405
Db 61 GTTGGCTTGAATCTCTTTGTTGACATCTTTGCTGTTGATTTGTTCTTGGTCACTTTTGG 120
QY 406 GAAGAGAAATAGATGATGAACGAATCCATCAGCCCTTGTGATTTGGGCTAGGCACTGGT 465
Db 121 GAAGAGAAATAGATGATGAACGAATCCATCAGCCCTTGTGATTTGGGCTAGGCACTGGT 180
QY 466 GTTACCAATTTGTTGATTAAGGAAAAAGCTCGCATCTCTCGTCTTTAGTGAAGAT 525
Db 181 GTTACCAATTTGTTGATTAAGGAAAAAGCTCGCATCTCTCGTCTTTAGTGAAGAT 240
QY 526 CTTTCTTCATATATCTTTTGGCCACCATTTATATTCATGACAGGGTTTCAAGTAAAGAG 585
Db 241 CTTTCTTCATATATCTTTTGGCCACCATTTATATTCATGACAGGGTTTCAAGTAAAGAG 300
QY 586 AAGCAGTTTTTCGGCAATTTCTGTAATTTATGCTTTTTTGGTGTCTTTGGGACTATTATT 645

Db 301 AAGCAGTTTTTCGGCAATTTCTGTAATTTATGCTTTTTTGGTGTCTTTGGGACTATTATT 360
QY 646 TCTTGACAAATCATATCTCTAGGTGTAAACACAGTTTCTTTTAAAGTTGGACATTTGAACC 705
Db 361 TCTTGACAAATCATATCTCTAGGTGTAAACACAGTTTCTTTTAAAGTTGGACATTTGAACC 420
QY 706 TTTGACTTGGGTGATTATCTTCTATTTGGTGCCATTTATTTGCTGCAACAGATTCAATATCT 765
Db 421 TTTGACTTGGGTGATTATCTTCTATTTGGTGCCATTTATTTGCTGCAACAGATTCAATATCT 480
QY 766 ACATGTCAGGTTCTGAATCAAGACGAGACACCTTTGCTTTTACAGTCTTGTATTCGAGAG 825
Db 481 ACATGTCAGGTTCTGAATCAAGACGAGACACCTTTGCTTTTACAGTCTTGTATTCGAGAG 540
QY 826 GGTGTTGTGAATGATGACCAAGCTCAGTTGTGTCTTCAACGCAATTCAGAGCTTTGATCTC 885
Db 541 GGTGTTGTGAATGATGACCAAGCTCAGTTGTGTCTTCAACGCAATTCAGAGCTTTGATCTC 600
QY 886 ACTCACTAAACCAAGAGCTGCTTTTCACTTTCTTGGAACTTCTTGTATTTGTTTCTC 945
Db 601 ACTCACTAAACCAAGAGCTGCTTTTCACTTTCTTGGAACTTCTTGTATTTGTTTCTC 660
QY 946 CTAAGTACCTTGGTGTGCTGCAACCGGTCTGATAAGTGCATGTTATCAAGAAGCTA 1005
Db 661 CTAAGTACCTTGGTGTGCTGCAACCGGTCTGATAAGTGCATGTTATCAAGAAGCTA 720
QY 1006 TACTTTGGAAGGCACTCAACTGACCGAGAGGTTGCCCTTATGATCTTATGCGGTATCTT 1065
Db 721 TACTTTGGAAGGCACTCAACTGACCGAGAGGTTGCCCTTATGATCTTATGCGGTATCTT 780
QY 1066 TCTTATATGCTTGTGAGCTTTTGCAGCTTGTAGCGGTATCCTCACTGTGTTTTTCTGTGT 1125
Db 781 TCTTATATGCTTGTGAGCTTTTGCAGCTTGTAGCGGTATCCTCACTGTGTTTTTCTGTGT 840
QY 1126 ATTGTGATGTCCATTTACATATGCGACAAATGTAAACGAGAGCTCAAGAAATACAAAG 1185
Db 841 ATTGTGATGTCCATTTACATATGCGACAAATGTAAACGAGAGCTCAAGAAATACAAAG 900
QY 1186 CATACCTTTGCAACTTTGTCATTTCTTGGGAGACATTTATTTCTTGTATGTTGGAATG 1245
Db 901 CATACCTTTGCAACTTTGTCATTTCTTGGGAGACATTTATTTCTTGTATGTTGGAATG 960
QY 1246 GATGCTTTGGACATTTGCAAGTGGAGATCCGTGAGTGAACACCCGGGAACATCGATCGCA 1305
Db 961 GATGCTTTGGACATTTGCAAGTGGAGATCCGTGAGTGAACACCCGGGAACATCGATCGCA 1020
QY 1306 GTGAGCTCAATCTTAATGGTCTGTGTCATGTTGGAAGACAGCGTTTGTCTTTCCGTTA 1365
Db 1021 GTGAGCTCAATCTTAATGGTCTGTGTCATGTTGGAAGACAGCGTTTGTCTTTCCGTTA 1080
QY 1366 TCGTTTCTTATCTTAACCTTAGCCAAAGAAATCAAGCGAGAAATCAACTTTTAAACATGAG 1425
Db 1081 TCGTTTCTTATCTTAACCTTAGCCAAAGAAATCAAGCGAGAAATCAACTTTTAAACATGAG 1140
QY 1426 GTTGTGATTTGGTGTGCTGCTCATGAGAGGTGCTGATCTATGGCTCTTGTGATACAAAC 1485
Db 1141 GTTGTGATTTGGTGTGCTGCTCATGAGAGGTGCTGATCTATGGCTCTTGTGATACAAAC 1200
QY 1486 AAGTTTCAAGGGCGGGCACAACAGATGTACCGGGAATGCAATCATGATCACGAGTACG 1545
Db 1201 AAGTTTCAAGGGCGGGCACAACAGATGTACCGGGAATGCAATCATGATCACGAGTACG 1260
QY 1546 ATAAGTGTCTGCTTTTGTAGCACAGTGTGTTGTTGCTGACCAACCACTCATAGC 1605
Db 1261 ATAAGTGTCTGCTTTTGTAGCACAGTGTGTTGTTGCTGACCAACCACTCATAGC 1320
QY 1606 TACCTATTACCGCACAGAACCCACACGAGCATGTTATCTGATGACAAACCCCAAAA 1665
Db 1321 TACCTATTACCGCACAGAACCCACACGAGCATGTTATCTGATGACAAACCCCAAAA 1380
QY 1666 TCCATACATATCCCTTTTGTGGACCAAGACTCGTTTATTGAGCCTTCAGGGAACCAAT 1725
Db 1381 TCCATACATATCCCTTTTGTGGACCAAGACTCGTTTATTGAGCCTTCAGGGAACCAAT 1440

Db 1853 TCCTCATGCGCCCCACACGAGCTGTCCACTATTAATCTGGAGACAGTTTGTGATGCGCTTCA 1912
Qy 1814 TGGACCCGCTTTTGGAGTGTGGGCTTTGTATCCCTTTGTTCAGAGTTCTCCAACTGAGA 1873
Db 1913 TGGCTCCTGTGTTGGTGGTGGGATTCGTTCCCTTTGTCCCTGCTCCGACTGAGA 1972
Qy 1874 GAACCCCTCCTGATCTTAGTAGGCTTGAAGGTGAAGGTGAAGAAAGCTT 1924
Db 1973 GAAGCAGCCATGATCTTAGTAACCTTGAAGAAAGATATATAGAAACTT 2023

RESULT 6

US-11-067-456-1

; Sequence 1, Application US/11067456
; Publication No. US20050144666A1
; GENERAL INFORMATION:
; APPLICANT: Blumwald, Eduardo
; APPLICANT: Apse, Marib
; TITLE OF INVENTION: INCREASING SALT TOLERANCE IN PLANTS BY
; FILE REFERENCE: OVEREXPRESSION OF VACUOLAR NA+/H+ TRANSPORTERS
; CURRENT APPLICATION NUMBER: US/11/067,456
; CURRENT FILING DATE: 2005-02-24
; PRIOR APPLICATION NUMBER: 10/155,535
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 09/271,584
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,474
; PRIOR FILING DATE: 1998-03-18
; PRIOR APPLICATION NUMBER: 60/116,111
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2136
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-067-456-1

Query Match 52.8%; Score 119.4; DB 24; Length 2136;
Best Local Similarity 81.5%; Pred. No. 83; 274; Indels 18; Gaps 2;
Matches 1362; Conservative 0; Mismatches 291;
Qy 272 AGAAGAGATAACAATGTTGGATCTCTAGTGTGGAACCTGCTTATCGATCGACATCTG 331
Db 353 AAAGAAAGATGACATGTTGCGCTCTTAACTCTAAATGCTATCGGTGCACTCTG 412
Qy 332 ATCAGCTTCTGTGGTGGTGGATCTCTTTGTTGCACTTCTTTGTTGCTTGTATGTTTC 391
Db 413 ATCAGCATCTGTGCTTCACTTAATCTCTTTGTTGCTTCTATGTTGCTTGTATCGTCA 472
Qy 392 TTGTCATCTTTTGAAGAGATAGATGATGATGATGATGATGATGATGATGATGATGATG 451
Db 473 TTGTCATCTTTTGAAGAGATAGATGATGATGATGATGATGATGATGATGATGATGATG 532
Qy 452 GGTAGGCACTGCTGTTACATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 511
Db 533 GGTAGGCACTGCTGTTACATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 592
Qy 512 TCTTAGTGAAGATCTTTTCTTCAATATCTTTTGGCCACCCATATATATCAATGAGGTT 571
Db 593 TCTTAGTGAAGATCTTTTCTTCAATATCTTTTGGCCACCCATATATATCAATGAGGTT 652
Qy 572 TCTTAGTGAAGATCTTTTCTTCAATATCTTTTGGCCACCCATATATATCAATGAGGTT 631
Db 653 TCTTAGTGAAGATCTTTTCTTCAATATCTTTTGGCCACCCATATATATCAATGAGGTT 712
Qy 632 TTGGCACTATTTTCTTCAATATCTTTTGGCCACCCATATATATCAATGAGGTT 691
Db 713 TTGGCACTATTTTCTTCAATATCTTTTGGCCACCCATATATATCAATGAGGTT 772
Qy 692 TGGCACTATTTTCTTCAATATCTTTTGGCCACCCATATATATCAATGAGGTT 751

Db 773 TAGACATTTGGGACCTTTGACTTTGGCGGATTTTCTTGGCAATCGCGCCCATATTTTGTGCAA 832
Qy 752 CAGATTCAGTATGTACTGCAAGTTCGAGTTCTGAATCAAGACGAGACACCTTTGCTTTACAGTC 811
Db 833 CGACTCTGTATGACACATCAAGTTCTCAATCAAGATGAGACACCTTTGCTTTACAGTC 892
Qy 812 TTGTATTCGGAGAGGTTGTGTGAATGATGCAACGTGAGTTGTGTGTCTTCAACGCGATTC 871
Db 893 TTGTATTTGGAGAGGCGTGTGTGAATGATGCAACGTGAGTTGTGTGTCTTCAATGCTATTC 952
Qy 872 AGAGCTTTGATCTCACTCACTTAACCAAGAGGCTTCTTTTCACTCTTCTTGAACCTTCT 931
Db 953 AGAGTTTGGACCTTCAACCACTTAACTATGAAGAGGCTTTTCAATTTCTTGGGAACCTTT 1012
Qy 932 TGTATTTGTTTCTTCTTAAGTACTTGTGTTGCTTGAACCGGTCTGATGAAGTGGTATG 991
Db 1013 TTTATCTGTTCTTGTGACACCGGACTTGTGTGCGAACTGTTCTGATGAGTGTATG 1072
Qy 992 TTATCAAGAGCTATATCTTTGGAAGGCACTCAACTGACGAGAGGTTGCCCTTATGATGC 1051
Db 1073 TCATCAAGAAACTGTATTTTGAAGGCACTCGACTGATCGAGAACTTGCCTCATGATGC 1132
Qy 1052 TTATGGCGTATCTTTCTTATATGCTTCTGAGCTTTTCACTTGTGAGCGGTATCCTCATG 1111
Db 1133 TTATGGCTTATCTTTCTATATATGCTTGTGAGCTATTCGCTTGTGATGCTTATCTTAACTG 1192
Qy 1112 TGTATTTCTGTGTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1171
Db 1193 TATTTTCTGTGGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1252
Qy 1172 GAATAACAACAAAGCATACCTTTGCACTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1231
Db 1253 GAAATTACTACCAAGCATGCTTGTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1312
Qy 1232 TGTATGTTGGAATGATGCTTGTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATG 1291
Db 1313 TCTACGTTTGAATGATGCTTGTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATG 1372
Qy 1292 GAAACATCGATCGAGTGTGATCACTTAAATGGGCTGCTGATGTTGTTGTTGTTGTTGTTGTTGTT 1351
Db 1373 GGACATGTTGCTGAGTGTGATCACTTAAATGGGCTGCTGATGTTGTTGTTGTTGTTGTTGTTGTT 1432
Qy 1352 TCGTCTTTCCGTTATCGTTTCTTCTTAACTTATAGCCAAAGAAATCAAAAGCGAGAAATCA 1411
Db 1433 TTGCTTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1492
Qy 1412 ACTTTAACTGAGGTTGTGATTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1471
Db 1493 GCATCAAGCAGCAAGTTGTGATCTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1552
Qy 1472 CTCTTGCATACAAAGTTTACAGGGCGGGGCAACAGATGTAACGGGATGCAATCA 1531
Db 1553 CTCTTGCCTCAATAGTTTACAGATCAGGGGCAACAGATGTAACGGGATGCAATCA 1612
Qy 1532 TGATCAGCAGTACGATTAATCTGTTCTTTTGTAGCAGTGTGTTGTTGTTGTTGTTGTTGTTGTTG 1591
Db 1613 TGATCAGCAGTACGATTAATCTGTTCTTTTGTAGCAGTGTGTTGTTGTTGTTGTTGTTGTTGTTG 1672
Qy 1592 AACCACTATAGCTTACCTATTTACCGACCAAGAGCGG-----CAACAGCAGCATGT 1642
Db 1673 AACCACTATAGCTTACCTATTTACCGACCAAGAGCGGCAACCAAGTACCAAGTATGT 1732
Qy 1643 TATCTGATGACAAACCCCAAAATCCATATATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1693
Db 1733 TATCTGATGACAAACCCCAAAATCCATATATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1792
Qy 1694 ACTGCTTCAATGAGCTTACAGGAAACCAATGTTGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT 1753
Db 1793 ATTCAATGAGTACCTGGGAGCCACAGGAGTGTGCAACCAAGCTTGGAGTT 1852
Qy 1754 TCTTGACACGCCCACTGCAACCGGTGATTTACTTGGAGCAATTTGATGATGATGATGATGATGATGATG 1813
Db 1853 TCTCATGCGGCCCAACAGGAGTGTCCACTATTTACTTGGAGACAGTTTGTGATGCTTCA 1912

Qy	1914	TGCACCCGCTCTTTGGAGGTCGTGGCTTTGTACCCCTTTGTCCAGCTTCTCCAACTGAGA	1873
Db	1913	TGCGTCTCGTGTGTTTGGTGGTGGCGGATTCGTTCCCTTTGTCCCTGGTCTCCGACTGAGA	1972
Qy	1874	GAACACCTCTCTGATCTTAGTAAGGCTTTGAGGGTAACTGGAAGAAAAAGCTT	1924
Db	1973	GAACGACCATGATCTTTAGTAAACCTTTGAGGAGAAAGATATATAGAAACTT	2023
RESULT 7			
US-11-067-558-1			
; Sequence 1, Application US/11067558			
; Publication No. US2005015510SA1			
; GENERAL INFORMATION:			
; APPLICANT: Blumwald, Eduardo			
; APPLICANT: Apee, Maris			
; TITLE OF INVENTION: INCREASING SALT TOLERANCE IN PLANTS BY			
; TITLE OF INVENTION: OVEREXPRESSION OF VACUOLAR NA+/H+ TRANSPORTERS			
; FILE REFERENCE: 529642000211			
; CURRENT APPLICATION NUMBER: US/11/067,558			
; CURRENT FILING DATE: 2005-02-24			
; PRIOR APPLICATION NUMBER: 10/155,535			
; PRIOR FILING DATE: 2002-05-24			
; PRIOR APPLICATION NUMBER: 09/271,584			
; PRIOR FILING DATE: 1999-03-18			
; PRIOR APPLICATION NUMBER: 60/078,474			
; PRIOR FILING DATE: 1998-03-18			
; PRIOR APPLICATION NUMBER: 60/116,111			
; PRIOR FILING DATE: 1999-01-15			
; NUMBER OF SEQ ID NOS: 27			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 1			
; LENGTH: 2136			
; TYPE: DNA			
; ORGANISM: Arabidopsis thaliana			
US-11-067-558-1			
Query Match 52.8%; Score 1149.4; DB 24; Length 2136;			
Best Local Similarity 81.5%; Pred. No. 6.3e-274;			
Matches 1362; Conservative 0; Mismatches 291; Indels 18; Gaps 2;			
Qy	272	AGAGAAGATAACAATGTTGGATTCTCTAGTGTGGAACCTGCCTTCGTTATCGACATCTG	331
Db	353	AAAGAAGAATGACAATGTTGCCTCTTTAACCTCTAAATGCTATCGGTGTCAACTCTG	412
Qy	332	ATCAGCTCTCTGTGGTTCGTTGAATCTCTTTGTTGCACTTCTTTTGCTTGTAATGTC	391
Db	413	ATCAGCATCTGTGTTTCACTTAATCTCTTTGTTGCCCTTCTATGCTTGATCGTCA	472
Qy	392	TTGTCATCTTTTGAAGAGATAGATGGATGAACGAATCCATCACCGCCTTGTGTAATG	451
Db	473	TTGCCCATCTTTTGGAGGAATCGATGGATAAAGCAATCCATCACTGCTTTATTGATG	532
Qy	452	GGCTAGGCACCTGGTGTACCAATTTTGTGATTAGTAAAGGAAAAAGCTCGCATCTCTCG	511
Db	533	GGCTTGGAATGCTGTGTCATATTTGATAGTAGAGGGAATACTCACATCTCTTGG	592
Qy	512	TCCTTAGTAGAATCTTTTCTTCATATATCTTTTGCAACCATATATATTCAAATCAAGGT	571
Db	593	TCCTTAGTAGAATCTCTCTTTATATATCTTTTGCCACCCATAATATTCATCGAGGT	652
Qy	572	TTCAAGTAAAAAAGACAGTTTTTCCGCAATTTTCGTACATTTATGCTTTTTTGGTCTG	631
Db	653	TTCAAGTAAAAAAGACAGTTTTTTCGAAATTTTGTAACTATTATGGCTTTTGGCGCA	712
Qy	632	TTGGGACTATTATTCTTTTGCAATCATATCTCTAGGTGTAAACAGTTCCTTTAAGAAGT	691
Db	713	TTGGGACGATGTTTCTTTGCAACCATATATCTCTAGGTGCAATTCAGTTCCTTTAAGAAAT	772
Qy	692	TGGACATTTGGAACCTTTGACTTTGGGTGATATCTTTGCTATTGTTGGTGCCTATTTGCTGCA	751
Db	773	TAGACATTTGGGACCTTTGACTTTGGCGCATTTTCTTTGCAATCGGGGCCATATTTGCTGCA	832

QY 1814 TCGACCCCTCTTTGGAGGTCGTGGCTTTGTATCCCTTTGTCCAGGTTCTCAACTGAGA 1873
DB |||||
1913 TCGGTCCTGTGTGGTGTGCGGANTCGTTCCCTTTGTCCCTGTCTCGACTGAGA 1972
QY 1874 GAAACCCCTCTGATCTTAGTAGAGGCTTGGAGGTAACGCTGGAAGAAAGCTT 1924
DB |||||
1973 GAAGCAGCATGATCTTAGTAACCTTGGAGGAAAGATATATAGAAACTT 2023
RESULT 8
US-10-425-114-20609
; Sequence 20609, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 20609,
; LENGTH: 1915
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3242-431-A12_FLI
US-10-425-114-20609
Query Match 38.4%; Score 837.4; DB 18; Length 1915;
Best Local Similarity 71.2%; Pred. No. 1.3e-196;
Matches 1143; Conservative 0; Mismatches 441; Indels 21; Gaps 2;
QY 294 TTCTCTAGTGTGCAAACTGCCCTTGGTATCGACATCTGATCAGCTTCGTGCTGCGTT 353
DB |||||
2 TTCTGTGTTTCAAAATGCAACGTTATCCACTCAGACCATGCTCGTGGTCTCCAT 61
QY 354 GAATCTCTTTGTGCACTCTTTGTGCTGTATGTTCTTGTGTCATCTTTTGGAAAGAA 413
DB |||||
62 GAATTAATTTGGCACTCTTTGTGTTGTTATGTTCTTGGCCATCTTTTGGAGAA 121
QY 414 TAGATGATGAACGAATCATCACCGCTTGTGTTGATGAGGCTAGGCACTGGTGTACAT 473
DB |||||
122 TCGATGGATGAACGAGTCTATCACTGCCCTTTTGTGTTGTTGCTGCTGGCTAGTCA 181
QY 474 TTGTTGATTAGTAAAGGAAAGCTCGCATCTTCTCGTCTTTAGTGAAGATCTTTCTT 533
DB |||||
182 TTGCTGTTTGTGTTGGCAAGGCTCAATATCTTGTGTTTCAAGTGAAGATCTTTCTT 241
QY 534 CATATATCTTTGCCACCACTATATTTCAATGACAGGTTTCAAGTAAAGAAAGCAGTT 593
DB |||||
242 TATATATCTTACCACTATAATATCAATGCCGGTTTCAAGTGAAGAAAGCAGTT 301
QY 594 TTTCCGAATTTGCTGACATATATGCTTTTGGTGTGTTGGGACATATATTTCTTGTGAC 653
DB |||||
302 TTTGTTAACTTCATGACCATCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 361
QY 654 AATCATATCTCTAGGTGAACAGTCTTTTAAAGTGTGACATTTGGAACCTTTGACTT 713
DB |||||
362 CATATACTTTGGTGGCCACAAATTTTAAAGGTTTGGATGTTGGTCTCTGGAAT 421
QY 714 GGGTGAATATCTTGTATTTGGTGCCATATTTGCTGCAACAGATTCAGTATGTACACTGCA 773
DB |||||
422 AGGGATTTCTTAGCAATTTGGTGAATATTTGCTGCAACGATTTCTGTTGCACTGCA 481
QY 774 GTTCTGAATCAAGCAGACACTTTGCTTTTACAGTCTTGTATTCGGAGAGGGTGTGT 833
DB |||||
482 GGTGCTAAATCAGGATGAGACACTTTGCTGTACAGTCTTGTATTTGGGGAGGGTGTGT 541

QY 834 GAATGATCAACGTCAGTTGTGTCTTCAACSCGATTCAAGCTTTGATCTCACTCACT 893
DB |||||
542 GAATGATCTACATCAGTGTGTCTTTCAATGCAATCCAAAGCTTTGACCTCAACCAAT 501
QY 894 AAACCAAGAGCTGCTTTTCACTTTTGGAAACTTCTGTATTTGTTTCTCTAAGTAC 953
DB |||||
602 TGACTCTTCAATTTGCTACACTTTTGGGAAATTTCTGTATCTATTTATCGCAAGCAC 661
QY 954 CTTGCTTGTGCTGCAACCGGCTGATAAGTGCATGTTATCAAGAGCTATCTTTGG 1013
DB |||||
662 AATGCTTGGAGTTTGGACAGGCTACTTAGTGTCTTACATTTAAAGAGCTGTACATGG 721
QY 1014 AAGCACTCAACTGACCGAGAGGTTGCCCTTATGATGCTTATGGGCTATCTTTCTTAT 1073
DB |||||
722 CAGGCACTCTACAGATCTGAGGTGCTCTTATGATGTTAATGGCATCTCTCTACAT 781
QY 1074 GCTTGTGAGCTTTTCGACTTGGAGCGGTATCTCACTGTGTTTCTGTGTTGTTGAT 1133
DB |||||
782 GCTTGTGAAATTTATGTTATCTGAGTGGCATTTCTCACTGTATTTCTTTTGTGTTGTTAT 841
QY 1134 GTCCATTTACATGCGCACATGTAAACGAGAGCTCAAGATTAACAACAGCATACCTT 1193
DB |||||
842 GTCTCATTTATACCTGGCATTAACGACGAGGTTCAAGATCTACTCAAGCATTTCTTT 901
QY 1194 TGCACCTTTGTCTTTCTTGGGAGACATTTATTTTCTGTATGTTGAAATGAGTGCCTT 1253
DB |||||
902 TGCAACCTTTGTCNTTTTGTGCTGAGATCTTTATCTTCTTTATGTTGTTGTTGTTGTT 961
QY 1254 GGCANTTCAAGTGGAGATCGTGAAGTGAACACCGGGAACATCGATGCGAGTGAAGTCT 1313
DB |||||
962 GGCATTTGAAAAATGGAATTTCTGAGTGTAGCCCTGGAACATCTGTAGCAACTAGTGG 1021
QY 1314 AATCCTAATGGTCTGCTCATGTTTGGAGAGCAGCGTTGCTCTTCCGTTATCCGTTCT 1373
DB |||||
1022 AGTATGTTGGTCTAAATTTCTTTTGGAGAGCAGCTTTGTTTTCCTCTTATCTCTCAT 1081
QY 1374 ATCTAACTTAGCAAGAAAGATCAAGCGAGAAATCACTTTAACTGACGAGTTGTGAT 1433
DB |||||
1082 ATCCAACTTGGCTAAAGAAATCAACAAATGAGAAATCAGCTTCAGACAGCAAGTATCAT 1141
QY 1434 TTGTTGCTGCTGCTCATGAGAGGTCGTATCTATGCTCTTGTGATCAACAAGTTTAC 1493
DB |||||
1142 TTGTTGGCTGGCTTATGAGAGGTCGTGTTTCAATCGCACTTGCATATAATCAGTTTAC 1201
QY 1494 AAGGCCGGGACACAGATGTACGGGGAATGCAATCATGATCAGAGTACGATCACTGT 1553
DB |||||
1202 CATGTCGGGGGACACTTTCACCTCGGAAGCAATGCAATCATGATCAAGCAACCATCACTGT 1261
QY 1554 CTGCTTTTATAGCACAGTGTGTTTGGTATGCTGACCAACCACTCATAGCTACCTATT 1613
DB |||||
1262 TGTGCTTTTACGACAGTGTGTTTGGTCTGTTGACTAAGCCATCATAGGCTTTTACT 1321
QY 1614 -----ACGCAACCAAGAGCCACCAAGAGCTGTTATCTGATGACCAACCC 1661
DB |||||
1322 GCCCATCTACTCCACATCAATAAGAAATCAAGCATCAGCATATCAAGATCCATCTACTCC 1381
QY 1662 AAATCCATATATCCCTTTTGGGACCAAGATCTGTTTCTTGTGAGCTTCTGAGGAA --- 1718
DB |||||
1382 AAGTCCAAATCAGTCACTATCCCACTTTCTGGGAGTCCCAAGAAATCTGAAGTTGATAT 1441
QY 1719 -----CCCAATGTGCTCGGCTGACAGTATAGTGGCTTCTTGACAGCGGCCACTCG 1772
DB |||||
1442 CGATGGCCATGATATTATCTGCTCAAGCAGTATTTGCTGCTTGTTCAGCTCCACACACA 1501
QY 1773 AACCGTCAATTACTACGAGACAAATTTGATGACTCTTTCATGCAACCGCTTTTGGAGG 1832
DB |||||
1502 CACTGTTTCTGTTGCGGTAAAGTTTGTATGATGATGCAATTCATGCTCTCTGTTTGGTGG 1561
QY 1833 TCGTGGCTTTGTACCTTTTGTTCAGGTTCTTCCAACTGAGAGAA 1877
DB |||||
1562 CAGGGGTTTGTGTTCTGTAGAACCTGGCTCCCACTGCAACCTGAACGTAA 1606

RESULT 9
US-10-424-599-58707
; Sequence 58707, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 58707
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MFT3847_24023C.1
US-10-424-599-58707

Query Match 37.7%; Score 821.8; DB 18; Length 1968;
Best Local Similarity 70.6%; Pred. No. 9.8e-193;
Matches 1134; Conservative 0; Mismatches 452; Indels 21; Gaps 2;

QY 292 GATCTCTAGTGTGAAAGCTGCTTCGTTATCGACATCTGATCAGCTTCTGTGTGCG 351
DB 16 GGTTCGTGTTTCAAAATGCAACGTTATCCACCTCAGACCATGCTCGTGTCTCC 75

QY 352 TTGAATCTCTTGTGTCATCTTGTGCTGTATGTTCTTGTGTCATCTTTTGGAAAG 411
DB 76 ATGAATCTTATTTGTGCGCATCTTCTTTGTGTTATGTTCTTGTGCGCATCTT 135

QY 412 AATAGATGATGAAGCAATCCATCACCCTGTTGTTGTTGTTGTTGTTGTTGTTGTT 471
DB 136 AATCGGTGATGACAGTCTATCTACTGCTCTTTGTTGTTGTTGTTGTTGTTGTTG 195

QY 472 ATTTTGTGTTAGTAAAGGAAAAAGCTCGCATCTTCTCGTCTTTTGTGTTGTTGTT 531
DB 196 ATTTTGTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 255

QY 532 TTCAATATCTTTTCCACCCCATATATCAATGACAGGTTTCAAGTAAAAAAGAACG 591
DB 256 TTATATATCTTCTACCACTATAATATTTAATGCGGGTTTTCAGGTGAAAAAAGAACG 315

QY 592 TTTATCCGCAATTCGTGACTATTATGCTTTTGTGTTGTTGTTGTTGTTGTTGTTG 651
DB 316 TTTTGTGTTTAACTTCATGACCATCATGTTGTTGTTGTTGTTGTTGTTGTTGTTG 375

QY 652 ACAATCATATCTCTAGGTGTAACACAGTTCTTTTAAAGAGTTTGGACATTTGGAAC 711
DB 376 ACCATCATAACTTTGGTGCCACACAAATTTTAAAGAGTTTGGATGTTGTTGTTG 435

QY 712 TTGGGTGATATCTGCTATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 771
DB 436 TTAGGGGATTTCTTAGCAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 495

QY 772 CAGGTTCGAAATCAAGACGAGACCTTTGTTTACAGTCTTGTATTCGGAGAGGTTG 831
DB 496 CAGGTGCTAAATCAGATGAGACCTTTGCTGTACAGTCTTGTATTTTGGGAGGG 555

QY 832 GTGAATGATGCAACGTGAGTTGTTGTTCTTCAACGCGATTCAGAGCTTTGATCTCA 891
DB 556 GTGAATGATGCTACATGAGTGTGTTTCTTCAATGCAATCCAAAGCTTTGACCT 615

QY 892 CTAACACGAGAGCTGCTTTTCTCTTCTTGTGAAACCTTCTGTTATTTGTTCTCT 951
DB 616 ATTGACTCTTCAATTTGCTGTACACTTTTGTGGGAAATTTCTTGTATCTATTAT 675

QY 952 ACCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1011

DB 676 ACAATGCTTGGAGTTTTCACAGGTTCTACTTAGTCTTACATTTATTAAGAGCTG 735
QY 1012 GGAAGGCACTCAACTGACCGAGAGGTTGCCCTTATGATGCTTATGCGGTATCTTCT 1071
DB 736 GGCAGGCACTCTACAGATCGTGAAGTTGCTCTTATGATGTTAAATGGCATACCTG 795
QY 1072 ATGCTTCTGAGCTTTTCGACTTTCGAGCGGTATCTCTACTGTTGTTTCTGTTG 1131
DB 796 ATGCTTCTGAAATGATGTTATCTGAGTGGCAATCTCTACTGTTATCTTTTGG 855
QY 1132 ATGTCCTCATACATGGCAATGTAACGAGAGCTCAAGAAATAACAAACAAACAT 1191
DB 856 ATGCTCTATATACCTGGCATACGTCAGAGAGTTCAAGAAATCACTACCAAGAT 915
QY 1192 TTTGCAACTTTTGTCAATTTCTTTCGAGACATTTATTTTCTTGTATGTTGGAAT 1251
DB 916 TTTGCAACCTTGTCTTTTGTGCTGAGATCTTTATCTTCTTATGTTGTTGTTG 975
QY 1252 TTGGACATTCGAAGTGGAGATCCGTGAGTGACACACGCGGAACATCGATCGAGTG 1311
DB 976 TTGGACATTCGAAATGGAATTTGTGAGTGATAGCCCTGGAACATCTGTAGCAAC 1035
QY 1312 TCAATCTTAATGGGTCTGGTTCATGTTTGAAGAGCAGGTTTCGTTCTTTCCTT 1371
DB 1036 TCAGCTTATTTCTGTCTAATTTCTTCTTGAAGAGCAGCTTTGTTTCCCTTAT 1095
QY 1372 CTATCTAACTTAGCAAGAGAAATCAAAAGCAGAGAAATCAACTTTTAAATGCA 1431
DB 1096 ATATCCAACTTTGGCTAAAAAATCAACAAATGAGAAAAATCAGCTTCAGAC 1155
QY 1432 ATTTGTTGTTGCTGCTCATGAGAGGTTGCTGATCTATGCTCTTGTGATACAA 1491
DB 1156 ATTTGTTGTTGCTGCTCATGAGAGGTTGCTGATCTATGCTCTTGTGATACAA 1215
QY 1492 ACAAGGCGCGGGCACACAGATGTACGCGGGAATGCAATCATGATCAGAGTAC 1551
DB 1216 ACCATGTCGGGGCACACTTCACTCGGAAGCAATGCAATCATGATCACAAGCA 1275
QY 1552 GTCTGTCTTTTATGACAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1611
DB 1276 GTTGTGCTTTTTCAGCACACAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1335
QY 1612 TT-----ACCGCACCAAGCACCACACGAGCATGTTATCTGTAGCAACACC 1659
DB 1336 CTGCCCCATCTCCACATCATAAAGAAATCAAGCATCAGATAATCAAGATCCAT 1395
QY 1660 CCAAAATCCATACATATCCCTTTGTTGGACCAAGACTCGTTTCATTTGAGCC 1718
DB 1396 CCAAGTCCAAATCAGTCACCTATCCCACTTCTTGGAGTGCCTCAAGAAATCT 1455
QY 1719 -----CCAAATGTCCTCGGCTGACAGTATAGTATAGTGTCTTTCAGG 1770
DB 1456 ATCGATGCCCATGATATTCATCGTCAAGCAGTATTCGTGCTTGTCTTACGAC 1515
QY 1771 CGAACCTGTGATTTACTACTGAGACAAATTTGATCTCTTTCATGCGGACCGCT 1830
DB 1516 CACACTGTTCACTGTTTGTGGCGTAAAGTTTGAATGATGATTCATGCTGCT 1575
QY 1831 GGTGCTGCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1877
DB 1576 GGCAGGGGTTTGTCTCTGTAGAACCTGGCTCACCACTGAACGTAA 1622

RESULT 10
US-10-369-324-38
; Sequence 38, Application US/10369324
; Publication No. US20030221213A1
; GENERAL INFORMATION:
; APPLICANT: ROMMENS, CAIUS
; APPLICANT: YE, JINGSONG
; APPLICANT: MENENDEZ-HUMARA, JAIME
; APPLICANT: YAN, HUA

APPLICANT: RICHARD, CRAIG
APPLICANT: BRINKHOFF, W. LEIGH
APPLICANT: SWORDS, KATHY M. M.
TITLE OF INVENTION: PRECISE BREEDING
FILE REFERENCE: 058951/0162
CURRENT APPLICATION NUMBER: US/10/369,324
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/357,661
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: 60/377,602
PRIOR FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 124
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 38
LENGTH: 1620
TYPE: DNA
ORGANISM: Solanum tuberosum
US-10-369-324-38

Query Match 36.6%; Score 797.6; DB 17; Length 1620;
Best Local Similarity 69.3%; Pred. No. 8.8e-187;
Matches 1101; Conservative 0; Mismatches 484; Indels 3; Gaps 1;

QY 287 TGTGGATCTCTAGTGTGGAACCTGCTTGGTATCGACATCTGATCAGGCTTCGTGG 346
DB 11 TGTGGCTTCTCTGTTTCCAAAACCTGGGCTCTTGGGTACTTTCAGATCATGCTTCTGTTG 70

QY 347 TTGCGTTGAATCTTTGTTGCACTTCTTTGCTTGTATGTTCTTGGTCACTTTTGG 406
DB 71 TATCAATCAACCTCTTTTGGCACTCTTTTGTCTTGCATCATCTTGTGTCATCTTGG 130

QY 407 AAGAGAAATAGATGATGAACGATCCATCACCGCTTGTGATGGGCTPAGGCACTGGTG 466
DB 131 AGGAGAACCGCTGGGTTATGAGTCCATCTGCTCCCTCATATTTGTTGTACAGAG 190

QY 467 TTACCAATTTGTTGATGATGAAGAAAGCTGCGCATCTTCTGCTTTTGTAGTGAATC 526
DB 191 TGGTTATCTTGTGCTGTAAGTGGTGGAAAGAACTCAACCTCTGCTTGTGTTTCACTGAAGATC 250

QY 527 TTTTCTTCATATATCTTTTGGCCACCATATATTCAGTCCAGGCTTCAAGTAAAGAA 586
DB 251 TCTTTTTCATATATGATGCTTCTCCCAATCATATTTAATGAGGCTTTCAGGTAAAGAA 310

QY 587 AGCAGTTTTTCCGCAATTTCTGCTATATGCTTTTGGTGTCTTGGGCACTATTTT 646
DB 311 AGCAATTTTGTGAACTTCATTAATGATGTTTGGAGCCATTTGTAACCTGGTCT 370

QY 647 CTTGCAATATATCTCTAGGTGTAACAAGTCTTTTAAAGATTTGGAATTTGAACCT 706
DB 371 CATGTGCCATATATCATTTAGGTGCAATTTCAAACTTTCAAGAAATTTGGACATTTGAATTC 430

QY 707 TTGACTGGGTGATATCTGCTATTTGGTCCATATTTCTGCTGCAACAGATTCAGTATGTA 766
DB 431 TAGATATGGGATATATCTGCAATTTGGAGCAATATTTGCTGCCACAGATTCGCTGCA 490

QY 767 CACTGAGGTTCTGAATCAAGAGAGACACCTTTGCTTTACAGTCTTGTATTTGGAGAG 826
DB 491 CATTGAGGTTCTGATCAGGATGAGACACCTCTCTTTACAGTCTTGTATTTGGAGAG 550

QY 827 GTTGTGTGAATGATCAACGCTCAGTTGTGCTTCAACGCGATTCAGAGCTTTGATCTCA 886
DB 551 GAGTTGTAATGATGCTACATCGTGGTGTCTTTCAATGCTATTTCAAACTTTGACCTTA 610

QY 887 CTCACCTAAACGAGAGCTCTTTTCATCTTCTGGAACTCTTGTATTTGTTTCTCC 946
DB 611 CGAGCGTGAATCCAGTATAGCCCTCAGTTCTCTTGGCAACTCTTCTATCTGTTCTTG 670

QY 947 TAAGTACCTTTGTTGGTCTGCAACCGGCTGATAGTGGTATGTTATCAAGAGCTAT 1006
DB 671 CTAGCACTTTACTGGGAGAGGAGCTGGTCTTCTTAGTGCTTACATTTCAAGAGCTGT 730

QY 1007 ACTTTGGAAGGCACTCAACTGACCGAGAGGTTGCCCTTATGATGCTTATGGGCTATCTTT 1066

DB 731 ATTTGGGAGGCACTCCACAGATCGTGAAGTTGCCCTTATGATGCTATGCTTACTTAT 790

QY 1067 CTTATATGCTTCTGCTGAGCTTTTCGAGCTTTGAGCGGTATCTCTACTGTGTTTCTGTGTA 1126

DB 791 CATACATGCTGGCTGAATTTCTATTGAGTGGGATTTCTACTGTATTTTCTGTGTA 850

QY 1127 TTGTCATGTCCATTAACAATGGCAATGTAACGAGAGCTCAAGAAATTAACAACAAGC 1186

DB 851 TTGTAATGTCTCATTAACAATTTGGCAATGTCAGGAGAGTTCAAGAGTCACTACAAGGC 910

QY 1187 ATACCTTTGCACTTTGCTTCTTGGGAGACATTTATTTCTTGTATGTTGGAATCG 1246

DB 911 ACGCTTTTGGCACTTTTGTCTTTTGGAGAGACTTCTCTCTTATGTGGGATGG 970

QY 1247 ATGCTTGGACATTCACAAGTGGAGATCGTGAAGTGAACACCGGAAACATGATCGCAG 1306

DB 971 ATGCTTTGGATATCGAAGTGGAAATTTGTTGGTGAACAGGCTGATTAATCAATTCG 1030

QY 1307 TGAGCTCAATCTTAATGGGTCTGTCATGTTGGAAGAGAGCGTTCGTCTTTTCCGTAT 1366

DB 1031 TGAGTTCAATATCTGATGGGATTAATCTTGTGGGAGAGCTGCTTTGTTTCCATTA 1090

QY 1367 CGTTTCTATCTAACTTAGCCAGAGAAATCAAGCGAGAAATCACTTTAATCATGCGAG 1426

DB 1091 CATCTTCTCAACTTAATGAAGAAATCTCGAGCAAAATAACCTTTAGGCGAG 1150

QY 1427 TTGTCATTTGGTGTCTGCTCTCATGAGAGGTGCTGATCTATGCTCTTGTGATCAACA 1486

DB 1151 TGATTAATGTTGGGAGGTTTGTATGAGAGGCGAGTGTCCATGCGCATGATTAATA 1210

QY 1487 AGTTTAAAGGCGCGGCAACAGATGTAACGCGGAATGCAATCATGATCAGAGTACGA 1546

DB 1211 AGTTCACTCGTGGGAGACACACTCACTGAGGCAATGCAATGATTAATGATTAACGAG 1270

QY 1547 TAACTGTCTGCTTTTATAGCAGTGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1606

DB 1271 TAACTATTTGTTTATTCAGCAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1330

QY 1607 ACCTATTACCGCAGCAGAACCGCACCGAGATGTTATCTGATGACAAACCCCAAAAT 1666

DB 1331 TCTGCTGCCACCAAGAGGCAATGAGTACAGTGTCTATGAGTGCATTAATCTCCAAAGT 1390

QY 1667 CCATACATATCCCTTTTGTGGAC---CAAGACTCGTTTCAATGAGCTTTCAGGGAACCA 1723

DB 1391 CTCTAACAGCCCCACTCTCTAGGAGTGCAGAGGACTCTGAAAGTTCATTTAAATGTTCCAG 1450

QY 1724 ATGTCCTCGGCTGACAGATATAGTGGCTTCTGACAGGCGCCACTCGAACCGTGCATT 1783

DB 1451 ATCTTCTCCACCCCAAGTTTGAGGATGCTACTTACCGCACCAAGTCAATAAGTGCATC 1510

QY 1784 ACTACTGGAGACAAATTCATGACTCCTTTCATGCGACCGCTCTTTGAGAGTCTGTCGCTTG 1843

DB 1511 GGTACTGGGAGGTTGACGATGATTCATGCGGCCCTATGTTGTTGTTGTTGTTGTTGTTG 1570

QY 1844 TACCTTTTGTTCAGGTTCTCCAACTGA 1871

DB 1571 CTCTCTGCTGCTGCTGCTTCTCCAACTGA 1598

RESULT 11
US-10-607-538-38
Sequence 38, Application US/10607538
Publication No. US20040107455A1
GENERAL INFORMATION:
APPLICANT: ROMMENS, CAIUS
APPLICANT: YE, JINGSONG
APPLICANT: HUMARA, JAIME M.
APPLICANT: YAN, HUA
APPLICANT: SWORDS, KATHY
TITLE OF INVENTION: PRECISE BREEDING
FILE REFERENCE: 058951/0167
CURRENT APPLICATION NUMBER: US/10/607,538
CURRENT FILING DATE: 2003-06-27

; PRIOR APPLICATION NUMBER: 10/369,324
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/357,661
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/377,602
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 38
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Solanum tuberosum
US-10-607-538-38

Query Match 36.6%; Score 797.6; DB 19; Length 1620;
Best Local Similarity 69.3%; Pred. No. 8.8e-187;
Matches 1101; Conservative 0; Mismatches 484; Indels 3; Gaps 1;

QY 287 TGTGGATTCTCTAGTGTGAAACTGCCCTTCGTTATCGACATCTCATCACGCTTCTGTGG 346
DB 11 TGTGGCTTCTCTGTTTCAAACTGGGCTCTTTGGGTACTTCAGATCATGCTTCTGTG 70
QY 347 TTGCGTTGAATCTTTGTGCACTCTTTGTGCTGTGTAATGTTCTTGGTCATCTTTTGG 406
DB 71 TATCCATCAACCTCTTTGTGGCACTCCCTTTGTGCTTGCATCATCTTGGTCATCTTGG 130
QY 407 AAGAAATAGATGATGAACGAAATCCATCAGCGCTTGTGATTTGGGCTAGGCACTGTG 466
DB 131 AGGAACCGCTGGGTTAATGAGTCCATTAATGCTCCCTCATTAATTTGGTTTGTGTACAGG 190
QY 467 TTACCACTTTGTGTTAGTAAGAAAGAAAGCTGCACTCTTCTGCTCTTTAGTGAAGATC 526
DB 191 TGGTTATCTGTCGTAAGTGTGGAAGAACTCACCTTCTGCTGTTTTCAGTGAAGATC 250
QY 527 TTTTCTTCATATCTTTTGGCACCATTATATCAATGCAAGGTTTCAAGTAAAGAAAGA 586
DB 251 TCTTTTTCATATATGTAATCTTCTCCCAATCATATTAATGCAAGGTTTTCAGGTAAAGAA 310
QY 587 AGCAGTTTTCGGAATTTCTGACTATATGCTTTTGGTGTGCTTGGGACTATTATT 646
DB 311 AGCAATTTTTCGTAAGTCTAATGAGTTCGAGGCCAATTTGGTACCCTGGTCT 370
QY 647 CTTCGACAAATCATATCTCTAGGTGTAACACAGTCTCTTAAAGAAAGTTGACATTTGGA 706
DB 371 CATGTGCCATTAATATCATATGAGTGCATTAACAACTTTCAAGAGTTGACATTTGAATTC 430
QY 707 TTGACTTGGGTGATATCTTGCTATTTGGTGCCATATTTGCTGCAACAGATTCAGTATGTA 766
DB 431 TAGATATTGGGATTAATCTTGCAATTGGAGCAATATTTGCTGCCACAGATTTCCGTCTGCA 490
QY 767 CACTGAGGTTCTGAATCAAGACGACACCTTTGCTTACAGTCTTGTATTCGGAGAGG 826
DB 491 CATTCAGGCTCTACATCAGGATGAGACACCCCTCTTTTACAGTCTTGTATTTGGAGAG 550
QY 827 GGTGTTGTAATGATGCAAGCTCAGTTGTGCTTCAACGCGATTTCAGAGCTTGTATCTCA 886
DB 551 GAGTTGTAATGAGTCAATCGGTGCTTCTTCAATGCTATTCAAACCTTTGACCTTA 610
QY 887 CTCACCTAAACCAAGAGCTGCTTTTCATCTTTCTTGGAACTCTTGTATTTGTTCTCC 946
DB 611 CGAGGCTGAATCCAGTATAGCCCTCAGTTTCTTGGCACTTCTTCTATCTGTTCCITG 670
QY 947 TAAGTACCTTGTGTTGGTGCACCGGTCTGATAAGTGCATGTTATCAAGAGCTAT 1006
DB 671 CTAGCACTTTTACTGGGAGCAGGAATGCTTCTTTAGTGCTTTACATTTATCAAGAGCTGT 730
QY 1007 ACTTTGGAAGGCACTCAACTGACCGAGAGTTGGCTTATGATGCTTATGGCTATCTTT 1066
DB 731 ATTTTGGCAGGCACTCCACAGATCTGAGGTTGGCTTATGATGCTCAAGCTTACTTAT 790
QY 1067 CTTATATGCTTGTGAGCTTTTTCGACTTGTGAGCGGTATCCTCACTGTGTTTTTCTGTGTA 1126
DB 791 CATACATGCTGGCTGAATCTTCTTATTTGAGTGGGATTTCTACTGTAATTTTCTGTGTA 850

QY 1127 TTGTGATGTCCCATTCACATGCGCACAAATGTACGGGAGAGCTCAAGATACACAAAGC 1186
DB 851 TTGTAATGTCTCATTCACATTTGGCACAATGTGACGGAGAGTTCAAGAGTCTCAACAGC 910
QY 1187 ATACCTTTGCAACTTTTCTTGGGAGACATTTATTTTCTTGTATGTTGGAATGG 1246
DB 911 ACGCTTTTGCACCTTTTCTTGTCACTTTTGGAGAGACTTTTCCCTTCTCTCTATGTCGGCATGG 970
QY 1247 ATGCTTTGGACATTTGACAAAGTGGAGATCCGTGAGTGAACACACCGGGAAACATCGATCGCAG 1306
DB 971 ATGCTTTGGATATCGAGAAGTGGAAATTTGTTGTTGAGAGCGCTGATTAATCAATTTCCG 1030
QY 1307 TGACTCAATCTTAATGGTCTGCTCATGTTGTTGAAAGAGAGCGTTGCTCTTTCCGTTAT 1366
DB 1031 TGAGTTCAATACTGATGGGATTAATCTTGTGGGGAGAGCTGCTTTGTTTTCATTTAT 1090
QY 1367 CGTTTCTATCTAACTTAGCCAAAGAAATCAAGCGGAGAAATCAACTTTTAAACATGCGAG 1426
DB 1091 CATTTCTTCCAACCTTAATGAAGAAATCCTCGGAGCAAAAATTAACCTTTAGGCGAGCAAG 1150
QY 1427 TTGTGATTTGGTGTCTGCTCATGAGAGGTGCTGTATCTATGGCTCTTGCATACAAACA 1486
DB 1151 TGAATAATATGTTGGGCAAGTTTGTATGAGAGCGCAGTGTCCATGGCACTGGCATATAATA 1210
QY 1487 AGTTTACAGGGCCGGGCGACACAGATGTACGGGGAATGCAATCATGATCAAGATFACGA 1546
DB 1211 AGTTTCACTCGTGGGGGACACACTCACTGCAGGACAAATGCAATTAATGATTAACGACGCA 1270
QY 1547 TAACTGTCTGTCTTTTATGACACAGTGTGTTGGTATGCTGACCAAAACCACTCATAAAGCT 1606
DB 1271 TAACCATTTGTTTATTCAGACAAATGTTTGGTTTAAATGACAAAACCTTTATATAGTC 1330
QY 1607 ACCTATTACCGCACCAAGCGCCACACGAGAGATGTTATCTGATGACAAACCCCAAAAT 1666
DB 1331 TCCTGTCTGCCACCACAGAGGCAATTTGAGTACAGTGTCTCATCAGGTGCAAACTACTCCAAGT 1390
QY 1667 CCATACATATCTCTTTTGTGAC---CAAGACTGTTTCATTTAGCCCTTCAGGGAAACACA 1723
DB 1391 CTCTAACAGCCCCACTCCTAGGCAGTCGAGAGGACTCTGAAGTTGATTTAAATGTTTCAAG 1450
QY 1724 ATGTGCTCTGGCTTCAGATATAGTGGCTCTTTGACACGCGCCCACTCGAACCCGTGCATT 1783
DB 1451 ATCTTCTTCAACCAACCAAGTTTGGAGTGTACTTTACGACCAAGTCATATAAGTGCATC 1510
QY 1784 ACTACTGAGACAAATTTGATGATCTCTTCATGCGACCCGCTCTTTTGGAGGTCGTGGCTTTG 1843
DB 1511 GGTACTGCGCAAGTTTGAAGATGCAATTCATGCGCCCTATGTTTGGTGGTGGGGAATTTG 1570
QY 1844 TACCTTTTGTTCAGGTTCTCCAACTGA 1871
DB 1571 CTCCTCTGCCCCCTGGTTCTCCACGGA 1598

RESULT 12
US-10-369-324-37
; Sequence 37, Application US/10369324
; Publication No. US20030221213A1
; GENERAL INFORMATION:
; APPLICANT: ROMMENS, CAIUS
; APPLICANT: YE, JINGSONG
; APPLICANT: MENENDEZ-HUMARA, JAIME
; APPLICANT: YAN, HUA
; APPLICANT: RICHARD, CRAIG
; APPLICANT: BRINKERHOFF, W. LEIGH
; APPLICANT: SWORDS, KATHY M. M.
; TITLE OF INVENTION: PRECISE BREEDING
; FILE REFERENCE: 058951/0162
; CURRENT APPLICATION NUMBER: US/10/369,324
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/357,661
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/377,602

;
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Solanum tuberosum
US-10-369-324-37

Query Match 36.5%; Score 794.4; DB 17; Length 1621;
Best Local Similarity 69.2%; Pred. No. 5.5e-186;
Matches 1099; Conservative 0; Mismatches 486; Indels 3; Gaps 1;

QY 287 TGTGATCTCTAGTGTGAAAGTCCCTTCGTTATTCGACATCTGATCAACGCTTCTGTGG 346
DB 11 TGTGCTTCTCTGTTTCCAAAGTGGCTCTTTGGGTACTTCAGATCATGCTTCTGTG 70

QY 347 TTGCGTTGAATCTCTTTGTTGCACTCTTTGTTGCTGTGATTTGTTCTGTGATCTTTGG 406
DB 71 TATCCATCAACCTCTTTGTTGGCACTCTTTGTTGCTTGTGATCATCATTTGTTGATCTCTTTGG 130

QY 407 AAGAGAAATAGATGTAAGCAATCCATCACCCTGTTGTTGATTTGGCTAGGCACTGTTG 466
DB 131 AGAGAAACCGCTGGGTTAATAGTCCATTTACTGCCCTCAATAATGTTGTTGTACAGGAG 190

QY 467 TTACCAATTTTGTGTTAGTAAAGGAAAGAGCTCGCATCTTCTCGTCTTTAGTGAAGATC 526
DB 191 TGGTTATCTTGTCTAGTAAAGTGGTGAAGAGCTCACACCTTCTGTTTTCAGTGAAGATC 250

QY 527 TTCTCTTCATATATCTTTTGGCAACCATATATATCAATGCAAGGTTTCAAGTAAAGAGA 586
DB 251 TCTTTTTCATATATGATCTTCTCAATCATATATTAATGCAAGGTTTTCAGGTAAGAGA 310

QY 587 ACAGTTTTCGCAATTTCTGACTATTTATGCTTTTGGTCTGTTGGACTATATTT 546
DB 311 AGCAATTTTTCGTAATTTCTTACTATTAATGTTTCGGAGCCATTTGTTACCTCGTCT 370

QY 647 CTTGCAATCATATCTCTAGGTGTAACAGGTTCTTTAAAGAGTTGGAATTTGGAACCT 706
DB 371 CATGTGCAATATATCATTTAGTGGCCATTTCAAACTTTCAAGAGTTGGCATTTGATTTTC 430

QY 707 TTGACTTGGGTGATATCTTGTATTTGGTCCATATTTGCTGCAACAGATTCAGTATGTA 766
DB 431 TAGATATTTGGGATATCTTTGCAATTTGGAGCAATATTTGCTGCCACAGATTCGGTCTGCA 490

QY 767 CACTGCAAGTTCTGAATCAAGACGACACCTTTGCTTTACAGTCTTTGTTATTCGAGAG 826
DB 491 CATTCGAGTCTTACATCAGSATGAGACACCCCTCTTTTACAGTCTTTGTTATTTGGAGA 550

QY 827 GTGTTGTGAATGATGCAACGCTCAGTTGTGCTCTTCAACGCGATTTCAGAGCTTTGATCTCA 886
DB 551 GAGTTGTAAATGATGCTACATCGTGTGCTTTTCAATGCTATTTCAAACTTCGACCTTA 610

QY 887 CTCACCTAAACCAAGAGCTGTTTTCATCTTTCTGGAACTCTGTTGATTTGTTTCTCC 946
DB 611 CGAGCATGAATCCAGTATAGCCCTCAGTTTCTTTGGCACTCTTCTATCTGTTCTTG 670

QY 947 TAAGTACCTTGTGTTGCTGCTGCAACCGGTTGATAGTGGTATGTTATCAAGAGCTAT 1006
DB 671 CTAGCACTTTTCTGGGAGCAGGAATGCTCTTTTAGTCTTTACATTTATCAAGAGCTAT 730

QY 1007 ACTTTGGAAGGCACTCAACTGACCGAGAGGTTGCCCTTATGATGTTATGGGCTATCTTT 1066
DB 731 ATTTTGGCAGGCACTCCAGATCTGAGGTTGCCCTTATGATGTTATGCTGCTTACTTAT 790

QY 1067 CTTATATGCTTGTGAGCTTTTTCGACTTCAGCGGTATCTCTACTGTTTCTGTTGTA 1126
DB 791 CATACTTGTGCGGAATTTATCTATTTTGTGAGGATTTCTACCGGTTTCTTCTGTTGTA 850

QY 1127 TTGTGATGTTCCATTTACATGTCACATGTCACAGTGAACGAGAGCTCAAGATAACAAAGC 1186
DB 851 TTGTAATGTTCTCACTACACTTGGCACAATGTGACGAGGTTTCAAGAGTCTACTAAGGC 910

QY 1187 ATACCTTTGCAACTTTTGTCAATTTCTTGGGAGACATTTATTTCTTGTATGTTGAATGG 1246
DB 911 ACACCTTTTGGCACTTTTGTCAATTTCTTGGAGAGACTTTCTCTCTCTCTATGTCGCGATGG 970

QY 1247 ATGCTTTGGACATTTGACAAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGAG 1306
DB 971 ATGCTTTGGATATCGAGAAAGTGGAAATTTGTTGGTGACAGGCTGGATATCAATTTCCG 1030

QY 1307 TGAGCTCAATCTCTAATGCTCTGCTGTTGTTGGAAGAGCAGCGTTCTGTTTCCGTTAT 1366
DB 1031 TGAGTTCAATCTCTAATGCTGAGTAAATCTTCTTGGGAGAGCTGCCCTTGTGTTTCCATTA 1090

QY 1367 CGTTTCTATCTAATCTTAGCAAGAGAAATCAAGCGAGAGAAATCAACTTTTAAATGCGAGG 1426
DB 1091 CATCTTATCAACTTAAATGAAGAAATCTCGGAGCAAAATTAACCTTTAGGCGAGCAAG 1150

QY 1427 TTGATATTTGGTGTCTGCTCATGAGAGGTCGTGATCTATGCTCTTGTGATCAACA 1486
DB 1151 TGATTAATATGTTGGGAGGTTTGTATGAGAGGCGCAGTGTCCATGCGCACTGGCATATA 1210

QY 1487 AGTTTACAAAGGCGCGGCGACACAGATGTACGCGGAATGCAATCATGATCACGAGTACGA 1546
DB 1211 AGTTTACCTGCTGGGAGACACACTCACTGCGAGGACATGCAATTAATGATTTACGAGACA 1270

QY 1547 TAACCTGCTGCTTTTTTAGCACAGTGTGTTGGTATGCTGACCAAAACCACTCATAAGCT 1606
DB 1271 TAACCATTTGTTCTATTTCAGCAAAATGTTATTCGGTTTAAATGACAAAACCCCTTTATAAGTC 1330

QY 1607 ACCTAATACGCAACAGAAACGCAACGAGATGTTATCTGATGACAAACCCCAAAAT 1666
DB 1331 TCCTGCTGCCACCAAGAGGCAATTTGAGTACAGTGTCTATCAGGCGCAAAATCTCCAAAGT 1390

QY 1667 CCATACATATCCCTTTGTTGGAC---CAAGACTCGTTTCATTGAGCCTTCAGGGAACCA 1723
DB 1391 CTCTAACAGCCCCACTCTCTAGGAGTGGAGAGACTCTGAAGTTGATTTAAATGTTCCAG 1450

QY 1724 ATGTCCTCGGCTGACAGTATACGTCGCTCTTTGACAGGCGCCACTCGAACCGTGCAAT 1783
DB 1451 ATCTCTCTCACCACCAAGTTTGGAGTGTCTACTTACCGCAAGTCTATAAGTGCATC 1510

QY 1784 ACTACTGAGACAAATTTGATGACTCTTTCATGCGACCCGCTCTTTGGAGGTCGTGGTTTG 1843
DB 1511 GGTACTGCGCAAGTTTTCAGCATGCTTTCATGCGCCCTATGTTTGGTGTGTCGGGATTTG 1570

QY 1844 TACCCTTTGTTCCAGGTTCTCCAACTGA 1871
DB 1571 CTCTCTCTGCTGCTGTTCTCAACGGA 1598

RESULT 13
US-10-607-538-37
; Sequence 37, Application US/10607538
; Publication No. US20040107455A1
; GENERAL INFORMATION:
; APPLICANT: ROMMENS, CAIUS
; APPLICANT: YE, JINGSONG
; APPLICANT: HUMARA, JAIME M.
; APPLICANT: YAN, HUA
; APPLICANT: SWORDS, KATHY
; TITLE OF INVENTION: PRECISE BREEDING
; FILE REFERENCE: 058951/0167
; CURRENT APPLICATION NUMBER: US/10/607,538
; PRIORITY FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 10/369,324
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/357,661
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/377,602
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 37
; LENGTH: 1621

[illegible]

Matches 1077; Conservative 0; Mismatches 487; Indels 6; Gaps 1;

```
QY 312 GCCTTCGTTATCGACATCTGATCAGCTCTCTGGTTGGTTGGTTGAATCTCTTTGTTGCACT 371
Db 329 GGTCTGTATACAGACTCCGACTACCGTTCGGTGGTGTCCATCAACCTGTTGTCGCGCT 388
QY 372 TCTTTGTTGTTGTTATTTGTTCTTGGTCACTTTTGGAGAGAAATAGATGGATGAACGAATC 431
Db 389 GCTTCGCGCTGCTGCTCTCGGCCACCTCTCGAGGAGAAATCGTGGGTCAATGAGTC 448
QY 432 CATCACCGCTTGTGTTGATTTGGCTAGGCACTGGTTACCATTTGTTGATTAAGTAAAGG 491
Db 449 CATCACCGCTGCTCATCATCGGCTCTGCAACCGCGTGGTATCTTGTGATGACCAAGG 508
QY 492 AAAAAGCTCGCATCTTCTCTCTTTAGTGAAGATCTTTTCTTCAATATCTTTTTCGCCAC 551
Db 509 GAAGAGCTCGCACTTATTCGTTCTTCACTGAGATCTCTTCTTCACTTACCTCTCTCTCC 568
QY 552 CAATATATTCATGCAAGGTTTCAAGTAAAGAAAGCAGTTTTCGCAATTTTCGTTGAC 611
Db 569 GATCATCTTCAATGCAAGTTTTCAGGTAAGAAAGCAATTTCTCCGGAATTTTCATGAC 628
QY 612 TATTATGCTTTTGGTCTGTTGGGACATTAATTTCTTGCAAAATCATATCTCTAGGTGT 671
Db 629 GATCAATTAATTTGGAGCGCTCGGGACAAATGATATCTTTTTCACAAATATCTATTGCTGC 688
QY 672 AACACAGTTCTTTAAGNAGTTCGACATTCGAACTTTGACTTTGGTGGTATTAATCTGCTAT 731
Db 689 CATTCGAATATTCAGCAGAAATGAACATTTGGAACGCTGGATGTAGAGATTTTCTTGCAAT 748
QY 732 TGGTGCCATTAATTTGCTGCAACAGATTCAGTATGTACACTGCAAGTTTTCGAATCAAGACGA 791
Db 749 TGAAGCCATCTTTTCTGCGACAGATTCCTGCTGCAATTTGCAAGTCTTCAATCAGGATGA 808
QY 792 GACACTTTGCTTTACAGTCTTGTATTCGAGAGGGTGTGTAATGATGCAAGTCACT 851
Db 809 GACACCTTTTGTACAGTCTGCTATTCGGTGAAGGTGTGTGAACGATGCTACATCAAT 868
QY 852 TGTGTTCTTCAACGGATTCAGAGCTTTGATCTCACTCACTAAACACGAGCTGCTTT 911
Db 869 TGTGTTCTTCAACGCACTACAGAACTTTGATCTTGCACATAGATGGGCTGTCTGTTCT 928
QY 912 TCATCTTCTTGGAACTCTTGTATTTGTTTCTCTTAAGTACCTTGTGTTGTTGCTGCAAC 971
Db 929 GAAATCTTGTGGGAACTCTTTTATTTATTTTGTGCGACCTCTCTTGGAGTATTGC 988
QY 972 CGGCTGATAGTGGTATGTTATCAAGAGCTATACCTTTGGAAGGCACTCAACTGACCG 1031
Db 989 TGGATTGCTCAGTGCATACATAATCAAGAAAGCTATACATTTGGAAGGCAATTTCTACTGACCG 1048
QY 1032 AGAGTTGCCCTTATGATGCTTATGCGGTATCTTTCTTATATGCTTGTGAGCTTTTCGA 1091
Db 1049 TGAGGTTGCCCTTATGATGCTCATGCTTACCTTTTCATATATGCTTGGCTGAGTTGCTAGA 1108
QY 1092 CTTGAGCGGTATCCTCAGTCTGTTTCTGTTGTTGTTGATGTGCTCCCAATTAACATGGCA 1151
Db 1109 TTTGAGCGGCACTTCTCAGCGTATCTTCTGTTGTTGTTGTAATGTACATTAACATTTGCA 1168
QY 1152 CAATGTAAAGGAGCTCAAGAAATTAACAAAGGATACCTTTTGAACACTTTGTCAATTTCT 1211
Db 1169 TAAAGTCAAGAGAGTTCAAGAGTTTACAAAGGACGCAATTTGCAACTCTGCTCTTCAT 1228
QY 1212 TCGGAGAGATTTATTTCTTATGTTGGATGATGCTTGGACATTCGAACTGAGTGGAG 1271
Db 1229 TGCTGAGACTTTTCTCTTCTGATGTTGGGATGATGATTTGGATATTTGAAATATGGGA 1288
QY 1272 ATTCGTTGAGTGACACACCGGGAACATCGATCGCAGTGAAGTCAATCTTAATGGGCTGGT 1331
Db 1289 GTTTCGAGTGACAGACCTGGCAATCCATTTGGGATAGCTCAATTTTGTAGGATTTGT 1348
QY 1332 CATGTTGGAAGAGAGCGGTTTCGTTCTTCGTTATTCGTTTCTATCTAACTTAGCCAAAGAA 1391
Db 1349 TCTGATTGGAAGAGTGTCTTTTGTATTTCCGCTGTCTTCTTGTGCGAACCTTAACAAAGAA 1408
```

```
QY 1392 GAATCAAAAGCGAGAAATCAACTTTAATCATGCAAGTTGTGATTTGTTGTTGTTGTTCTCAT 1451
Db 1409 GGCACCGATGAAAAAATAAATCTGGAGACAGCAAGTTGTATATGTTGGCTTGGGCTGAT 1468
QY 1452 GAGAGGTCTGTATCTATGCTTCTTGCATACAAAGTTTCAAGGGCGGCGACACAGA 1511
Db 1469 GAGAGGAGCTGTGCTGATTTGCTTCTTCAATTAAGTTTACAGATCTGGCCATCTCA 1528
QY 1512 TGTACGGGGATGCAATCATGATCAGAGTACGATAACTGTCTCTTTTATAGCACGT 1571
Db 1529 GCTGACCGCAATGCAATTAATGATCACCAGCACCATCTGCTGTTCTTTTAGCACTAT 1588
QY 1572 GGTGTTTGGTATGCTGACCAAAACCACTCATTAAGCTTACCTATTACCGCACAGAACGCCAC 1631
Db 1589 GGTATTTGGGATGATGACAAAGCCATTGATCAGGCTGTGCTACCGGCTCAGGCGCATCC 1648
QY 1632 CACGAGCATGTTATCTGATGACAAACACCCCAAAATCCATACATATCCCTTTGTTGGAACA 1691
Db 1649 TGTACC-----TCTGAGCCTTCATCACAAAGTCCCTGCAATCTCTCTCTGACAAG 1702
QY 1692 AGACTCGTTTCTATGAGCCTTCAGGGAACCAATGTGCTCGGCTGACAGTATACGTGG 1751
Db 1703 CATGCAAGTTTCTGACCTCGAGAGTACAAACCAATTTGTGAGGCTTCCAGCCTCCGGAT 1762
QY 1752 CTTCTTGACCGGCCACTCGAAACGTCATTTACTTACTGGAGACAAATTTGATGACTCTTT 1811
Db 1763 GCTCTCACAGCGCGACCCACATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1822
QY 1812 CATGCAACCGCTTTTGGAGGTCGTGCTTTGTACCTTTTGTTCAGGTTCTTCAACTGA 1871
Db 1823 GATGCGCGGATGTTTGGCGGGGGTGTGTCCTTCTGCTCTTCTTCTTCTTCTTCTTCTTCT 1882
QY 1872 GAGAAACCTT 1881
Db 1883 GCGAGCCAT 1892
```

RESULT 15

US-10-155-535-3

; Sequence 3, Application US/10155535

; Publication No. US20030046729A1

; GENERAL INFORMATION:

; APPLICANT: Blumwald, Eduardo

; APPLICANT: Adee, Marie

; TITLE OF INVENTION: INCREASING SALT TOLERANCE IN PLANTS BY

; FILE REFERENCE: 529152000720

; CURRENT APPLICATION NUMBER: US/10/155,535

; CURRENT FILING DATE: 2002-05-24

; PRIOR APPLICATION NUMBER: 09/271,584

; PRIOR FILING DATE: 1999-03-18

; PRIOR APPLICATION NUMBER: 60/078,474

; PRIOR FILING DATE: 1998-03-18

; PRIOR APPLICATION NUMBER: 60/116,111

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 2066

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-10-155-535-3

Query Match

Best Local Similarity 33.0%; Score 719; DB 14; Length 2066;

Matches 1056; Conservative 0; Mismatches 540; Indels 3; Gaps 1;

```
QY 326 CATCTGATCAGCTCTGTTGCTTGGTTGATCTTTGTTGCACTCTTTGTTGCTTCTTGTGCTGTA 385
Db 50 CTTCTGATCATGATCGGTCGTCTCCATGAATTTGTTGCTAGCTTTGTTGCTTGTGCTTGTGA 109
QY 386 TTGTTCTTGGTCACTCTTTTGGAAAGAGATAGATGATGAACGAATCCATCACCGCTTGT 445
```

Db 110 TCGTCTTGGTCACTTGTGAGGAGACTCGGTGATGAACAGTCAATCACTGCTCTTA 169
Qy 446 TGATTTGGCTAGGCACTGGTGTATACATTTTGTGATTAAGTAAAGGAAAAAGCTCGCATC 505
Db 170 TCATTGGTTCGTGTACTGGGATTTGTGATCTTGTCTTATAAGTGGAGGAAAAGCTCAAGGA 229
Qy 506 TTCCTGCTTTAGTGAAGATCTTTTCTTCATATATCTTTTGGCCACCCATTATATTCATATG 565
Db 230 TTCCTTGTGTAGTGAAGATCTCTCTTTATTTATTTATCTTCTCCACCAATTATATTCACG 289
Qy 566 CAGGGTTTCAAGTAAAGAAAGACAGTTTTCGCAATTTCTGCTGACTATTATGCTTTTGTG 625
Db 290 CAGGGTTTCAAGTAAAGAAAGACAAATTTTTCGCACTTTCATGACCATTATGATTTTGTG 349
Qy 626 GTGCTGTTGGCACTAATATTTCTTGCAAAATCATATCTCTAGGTGTAAACAGTTTCTTTA 685
Db 350 GTGCTATTTGGAACCTCTCATTTTCAITTTGTTATCATCTCATTTTGGTGTAAACATCTTTTCG 409
Qy 686 AGAAGTTGGACATTTGGAAACCTTTGACTTTGGGTGATTATCTTGCTATTTGGTGCCATATTTG 745
Db 410 AGAAATGAATATCGGTGATCTTACCAATTGGGACTATCTAGCCCAATTGGAGCAATATTTCT 469
Qy 746 CTGCAACAGATTCAGTATGTACACTGAGGTTCCTGAATCAAGACGAGACACCTTTGCTTTT 805
Db 470 CTGCTACAGACTCTGTTTGCACCTTGCAGTGTCTTAATCAAGACGAGACACCTCTCTGT 529
Qy 806 ACAGTCTTTGATTCGGAGAGGGTGTGTGAATGATGCAACGCTCAGTTGTGCTTTCACAG 865
Db 530 ACAGTCTTTGCTTTGGAGAAGGTGTAGTGAAGCATGCCACATCGGTGCTCTTCAATG 589
Qy 866 CGATTCAGAGCTTTGATCTCACTCACTTAACACGAGAGCTGCTTTTCATCTTCTTGAA 925
Db 590 CAATAACAGAGATTCGACCTCAAAATATCAATTCAGCCATAGCTTTGGAGTTTGTCTGAA 649
Qy 926 ACTTCTGTATTTTGTCTCTTAAGTACCTTGTGCTGCTGCAACCGTCTGATTAAGTG 985
Db 650 ACTTTTGTATCTCTTTTATCTTAAGCACAGACCTTGTGTTGCGAGCTGGATGCTCAGTG 709
Qy 986 CGTATGTTATCAAGAAGCTATATCTTTGGAAGGCACTCAACTGACGAGAGGTGTCCCTTA 1045
Db 710 CTTTGTGTTATCAAGAAGCTATATATAGGAAGGCACTCTACTGATCGTGAAGTTGCACITTA 769
Qy 1046 TGAAGCTTATGGCGTATCTTTCTTATATGCTTGTGAGCTTTTCGACITTAGCGGTATCC 1105
Db 770 TGANGCTATTTGGCTTACTTATCATATATGTTGGCAGAGCTATTCACCTTGAGCTCTATCT 829
Qy 1106 TCACCTGTGTTTTCGTGCTATTTGTGATGTCCCAATTACATGCGACAAATGTAAACGGAGA 1165
Db 830 TGACTGTGTTCTTCTGCGGGATTTGTATGTCTCACTATACATGGCACAAATGTTACAGATA 889
Qy 1166 GCTCAAGAAATACAAACAAAGCATACCTTTGCAATCTTTGCTCATTTCTTGGCGAGACATTTA 1225
Db 890 AATCAAGGTCACTACAAACACATACTTTTGTGCAATGTCTATTTCTAGCTGAGATTTTTA 949
Qy 1226 TTTTCTTGTATGTTGGATGATGTCCTTTGGACATTTGACAGTGGAGATCCGTTGAGTGACA 1285
Db 950 TCTTCTTTTACGTTGGAAATGGAAGCTCTCGATATCGAGAAATGGGACGTTGTATCGCAACA 1009
Qy 1286 CACCGGGAACATCGGATCCAGTGAAGCTCAATCTTAATGGGTCTGGTCAATGTTGGAGAG 1345
Db 1010 GTCTTGGTTCAGTCGATTTGAGTTAGTTCAATACTCTTTTGGGCTTATCTTCTGGGTGCG 1069
Qy 1346 CAGCGTTTCGTTTCCGTTATCGTTTTCTATCTAAGCTTAGCCAAAGAAATCAAGCGGAGA 1405
Db 1070 CCGCGTTTCGTTTCCACTTTCTTCTTGTCCAAATTTAAACAAAGTCTTTCACCGGATGAGA 1129
Qy 1406 AAATCAACTTTTAAACATGACGTTGTGATTTTGGTGTCTGGTCTCATGAGAGGTGCTGTAT 1465
Db 1130 AAATAGACTTTAAAGAAACAAAGTAAACCAATTTGGTGGGCTGGTCTGATGCGTGTGCAGTGT 1189
Qy 1466 CTATGGCTCTTTGCATACAAAGTTTACAAAGGCGCGGACACAGATGTACGCGGGAATG 1525

Db 1190 CAATGGCTCTTGTCTTATAACAGTTTCACACTTCAGGACACACCAAGGTTCTTGGGAACG 1249
Qy 1526 CAATCATGATCACAGTACGATAACTGTCTGTCTTTTATAGCACAGTGGTGTGTTGATGC 1585
Db 1250 CTATCATGATCACAGTACCATCACTGTGTCTTTTTCAGTACTGTGTGTTTGGATGTC 1309
Qy 1586 TGACCAACCACTCATTAAGCTACCTATTAACGACCAAGAACCCACCAAGAGCATGTTAT 1645
Db 1310 TAACCAAAACCGTTAGTCAAAATTTGAGGCTTTCATCAAAACAGTCTCTCAACGACCGGC 1369
Qy 1646 CTGATGACAAACACCCCAAAATCCATACATATCCCTTTGTTGGACCAAGACTCGTTTCATTG 1705
Db 1370 TGCAGATCACACTAAGATCTTCTTTCCAGATCCGATCCTCCATGAGCGGTTGCTCAGTA 1429
Qy 1706 AGCCTTCAGGGAACCACAATGTGCTCT---CGGCCCTGACAGTATACGGTGGCTTCTTGACAC 1762
Db 1430 CCCAAGGCCAGTCAAGAAATACGACCTGAAACAACATGTTAGCTTCAGAAATGTTCTGGAAT 1489
Qy 1763 GGCCCACTCGAACCGTGCATTTACTCTGAGACAAATTTTGATGACTCCTTCATGCGACCG 1822
Db 1490 CTCGTCAGGGCCATTCATCAITTTACTGGAGGAAATTCGATAACGCAAGTTATGCTGCGCA 1549
Qy 1823 TCTTTGGAGGTCTGTGGCTTTGTACCTTTTGTTCAGGTTCTCCAACTGAGAGAAACCTC 1882
Db 1550 TATTTGGTGGCGAGGGGTTTCCACAGTAGTTCCAGGTTCAACCCATTGAGAAATAGTGTTC 1609
Qy 1883 CTGATCTTTAGTAAGGCTTGAGGGTAACTGAGGTAACGTGGAAGAAAG 1921
Db 1610 CGCAATGGAGTGAAGAAGTAGAAAAACAAGGAACAAACG 1648

Search completed: August 28, 2005, 11:19:29
Job time : 1444 secs


```
Db 793 TTTCTTCATTTACCTTCTCCACCGATCATTTTAAATGCTGGGTTCCAGGTGAAAAGAAA 842
QY 589 CAGTTTTCCGCAATTCGTGACTAATATGCTTTTTGGTGTGTTGGGACTATTAATTTCT 648
Db 843 TCATTTCTTCGCAATTCAGTACTATCATGCTCTTTGGGCGAGTTGGCACCTTGATATCG 902
QY 649 TGCACATCATATCTCTAGGTGTACACAGTCTTTTAAGAAGTTGGACATTTGGAACCTTT 708
Db 903 TTCATTTATATACGCGGGTCTATTGGCAATTTTCAAGAAAATGGATATTTGGACACCTT 962
QY 709 GACTTTGGGTGATTAATCTTGCTAATGCTGCCATATTTGCTGCAACAGATTCAGTATGTACA 768
Db 963 GAAATTTGAGATTAATCTTGCAATTTGGAGCAATCTTTGCTGCAACAGATTCGTATGCAAC 1022
QY 769 GTGAGGTTTCTGAATCAAGACGAGACACCTTTGCTTTTACAGTCTTTGTTATTCGGAGAGGT 828
Db 1023 TTTACAAGTCTTAAATCAGGAAGAACACCGTTATTGTACAGTCTAGTGTGTTGGAGAAGT 1082
QY 829 GTTGTGAATGATGCAACGTCAGTTGTGCTTTCAACGCGAATTCAGAGCTTTGATCTCACT 888
Db 1083 GTTGTGAATGATGCAACGTCAGTTGTGCTTTCAATGCTGTCCAGAACTTTGACTTATCT 1142
QY 889 CACCTAAACACGAGCTGCTTTTCATCTCTTGAAACTTCTGTAATTTGTTTCTCCTA 948
Db 1143 CATATCAGCAGGCAAGCTCTGCAATTAATTTGAAACTTCTATATCTTTGCTGCTCG 1202
QY 949 AGTACCTTCTGTTGCTGCAACCGGTCGTGAATGAGTGTGTTATCAAGAAAGCTATAC 1008
Db 1203 AGCACTTCTTAGGGGTTGCTGTTGSCCTACTAAGTGCCTTTATAATTAAGAACTCTAC 1262
QY 1009 TTTGGAAGGCACTCAACTACGAGAGGTTGCCCCTTATGATGCTTTATGGCGTATCTTTCT 1068
Db 1263 TTTGGAAGGCACTCAACTGATCGTGAAGTTGCTAATTAATGATACTCATGCGCGTACATCA 1322
QY 1069 TATATGCTTGTGAGCTTTTGACCTTTGAGCGTATCTCTCACTGCTGTTTTCTGTGGTATT 1128
Db 1323 TACATGCTTGTGAATTAATCTATTTAAGTGGAACTCTCACTGCTGTTTTCTGTGGGATC 1382
QY 1129 GTGATGTCCTCAATACACATGGCACAATGTAAAGGAGCTCAAGAAATACAAACAGCAT 1188
Db 1383 GTGATGTCCTCAATACCTGGCATTAATGTGACTGAGAGCTCAAGAGTCACTACCAAGCAC 1442
QY 1189 ACCTTTGCAACTTTGTCATTTCTCGGAGACATTTATTTCTGTATGTTGGATGAT 1248
Db 1443 ACGTTTGTCTACATTAATCAATTTATGCTGAAATTAATCATATTTCTTATTTGTTATGGAT 1502
QY 1249 GCTTTGGACATTCACAAGTGGAGATCCGTTGAGTGACACACCGGGAACATCGATCGAGTG 1308
Db 1503 GCTTTGGACATTCAGAAGTGGAAAGTTTGAAGCGACAGCCCGGAACATCAATTAAGTGC 1562
QY 1309 AGCTCAATCTTAATGGGTCGTGCTATGTTTGGAGAGCAGCGTTCGTCTTTCCGTTATCG 1368
Db 1563 AGCTCAATCTCTGCTAGTCTGTTTGGTTGGAGGGAGCCTTTGTTTCCCTTTGTCA 1622
QY 1369 TTTCTATCTAATGACCAAGAAATCAAGCGAGAAATCAACTTTAAATGACAGGTT 1428
Db 1623 TTTCTGTCCAACTTGACCAAGAAATCCTGAGGCAAGAATAGCTTTAAACGAGCAGGTT 1682
QY 1429 GTGATTTGTTGCTGCTCATGAGAGTGTCTATCTATGGCTCTTGGCATACAAACAG 1488
Db 1683 ACAAATGTTGGGCTTATGCGAGTGTCTGTTCTATGCGCCCTTGTCTTATATCAG 1742
QY 1489 TTTACAAGGGCGGGGCAACAGATGTACGCGGAAATGCAATCATGATCACGAGTACGATA 1548
Db 1743 TTTACAAGGGAGGTCATCTACTCAGTTACGTGCAATGCAATAATGATCACGAGTACTATC 1802
QY 1549 ACTGTCGTCTTTTATGACAGTGTGTTTGTGATGCTGACCAACCC---ACTCATAGC 1605
Db 1803 ACTGTTGCTCTTTTACAGACAGTGTGTTTGTGTTGATGACAAAACCTTTAATCTATTA 1862
QY 1606 TACCTATTACCGCACAGAACCCACGAGCATGTTATCTGATGACACAAACCCCAAAA 1665
```

RESULT 2

```
US-09-830-123-14
; Sequence 14, Application US/09830123
; Patent No. 6803500
; GENERAL INFORMATION:
; APPLICANT: Iida, Shigeru
; APPLICANT: Tanaka, Sachiko
; APPLICANT: Inagaki, Yoshihide
; TITLE OF INVENTION: Genes Encoding Proteins Regulating the pH of Vacuoles
; FILE REFERENCE: 001560-397
; CURRENT APPLICATION NUMBER: US/09/830.123
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: PCT/JP00/05722
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: JP 11/236800
; PRIOR FILING DATE: 1999-08-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 2423
; TYPE: DNA
; ORGANISM: Petunia hybrida
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(2423)
; OTHER INFORMATION: Nucleotide sequence of DNA encoding for protein regulating the
; OTHER INFORMATION: pH of vacuoles
US-09-830-123-14
```

Query Match 37.3%; Score 813; DB 4; Length 2423;

Best Local Similarity 70.6%; Pred. No. 2.5e-197; Mismatches 455; Indels 3; Gaps 1;

Matches 1099; Conservative 0;

QY 318 GTTATCGACATCTCATCGCTCTCTGTGGTTGCGTGAATCTCTTTGTGCACTTCTTTG 377

Db 393 GTTATCGACATCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 452

QY 378 TGCCTGTATTGTTCTTGGTCACTCTTTTGGAGAGATAGATGATGATGATGATGATGATGAT 437

Db 453 CGCGTGTATTGTGATCGGTCACTTTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 512

QY 438 CGCCTTGTGATTTGGGCTAGGCACTGGTGTACCATTTTGTGATTAAGTAAGGAAAG 497

Db 513 TGCCTTAGTGATTTGGTCTTGTGATCTGGAATCGTTATTCTACTGATAAGTGGAGAAAGAA 572

QY 498 CTCCGATCTTCTCGCTTTTAGTGAAGATCTTTTCTTCATATACTTTTGGCCACCATAT 557

Db 573 CTCTCATATTTTAGTGTTCAGTGAAGATCTTTTCTTCTTATTTACCTTCTTCGCAATCAT 632

QY 558 ATTCAATGCGAGGTTTCAAGTAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 617

Db 633 TTTTAATGCTGGGTTCCAGGTGAAAAAGAAATCGTTCTTCGCAATTTTTCAGCATCATCAT 692

QY 618 GCTTTTGGTCTGTTGGGACTATTATTCTTTCGCAATCATATCTCTAGGTGTAACACA 677

```
Db 693 GCTCTTTGGGCACTTGGCACCTTGATATCATTTATTTATATCATTTAGTGCCATTGG 752
Qy 678 GTTCTTTAAGAAAGTTGGACATTTGGAACTTTTGCATTTGGGTGATTTCTTGTATTGGTGC 737
Db 753 CATTTTCAAGAAATGAATTTTGGAACTTTGAATTTGAGATTAACCTTTGCATTTGGGCG 812
Qy 738 CATATTTGCTGCAACAGATTCAAGTATGTAACCTGCAAGTTTCTGAAATCAAGACGACACACC 797
Db 813 AATCTTCTGCTACAGATTTCTGATGCACTTCAAGTGTCTTAATCAGGATGAACACACC 872
Qy 798 TTTGCTTTTACAGTCTTGTATTTCCGAGAGGGTGTGTGAATGATGCAACGTCAAGTTGTGGT 857
Db 873 CTATTTGTACAGTCTAGTTTGTGGGGAAGGTGTGTGAATGATGCAACATCTGTAGTTCT 932
Qy 858 CTTCAACGGGATTCAGAGCTTTGATCTCACTCACTTAAACCAACGAAAGCTGCTTTTCACT 917
Db 933 GTTCAATGCTATCCAGACTTTGATCTTATCTCACTCAACGCGGAAGCTATGGAATTT 992
Qy 918 TCTTGGAACTTCTTGTATTTGTTTCTCTAAGTACCTTGTGTTGGTGTGCTGCAACCGGTCT 977
Db 993 AGTTGGAACTTCTTATATCTTGTGCTCAAGCACTGCCCTAGGAGTTGCTGTGGCT 1052
Qy 978 GATAAGTGGTATTTATCAAGAGCTATACCTTTGGAAGGCACTCAACTGACCGAGAGGT 1037
Db 1053 ACTGAGCGCTATATTTATTAAGAACTCTACTTTGGAAGGCACTCAACTGACCGTGAAGT 1112
Qy 1038 TGCCCTTATGATCTTATGGCGTATCTTCTTATATGCTGTGAGCTTTTTCGACTGAG 1097
Db 1113 TGCTATATGATPACTCATGGCTTACTATCTTACATGCTTGTGTAATTTCTATTAAAG 1172
Qy 1098 CGGTATCTCTACTGTGTTTTCTGTGATTTGTGATGTGCCATTTACATATGSCACAATGT 1157
Db 1173 TGCAATCTCTACTGTGTTTTCTCTGGGATGCGATGCTCACTACACTGGCAATGT 1232
Qy 1158 AACGAGAGCTCAAGAAATACAAAGCAATCACTTTGCAACTTTGTCAATTTCTTGCGGA 1217
Db 1233 GACTGAGAGCTCGAGAGTCACTTACCAGCACACTTTTGTCTACATTTATTTATTTGCTGA 1292
Qy 1218 GACATTTATTTCTTGTATTTGGAATGATGCTCTTGGACATTTGACAAAGTGGAGATCGT 1277
Db 1293 AATATTCATTTCTTATTTGTTGATGATGCTTTGGACATTTGAGAGTGGAAATTTGT 1352
Qy 1278 GAGTGACACACCGGGAACATCGATCGCAGTGAAGTCAATCTTAAATGGGTCTGGTCAATGGT 1337
Db 1353 AAGCCAGCCCTGGAAATACAGTTTCAAGTTAGCTCAATATTTGCTGGGTCTTGTTTGGT 1412
Qy 1338 TGGAAAGAGAGCGTTTGGTCTTTCCTTATCGTTTCTATCTAATTTAGCCAAAGAAATCA 1397
Db 1413 TGGAAAGAGCAGCATTTGTTTTCCTATTTGCCATTTGTCTTGTCCAACTTTGACCAAGAACTCC 1472
Qy 1398 AAGCCAGAAATCAACTTTTAACTGACGTTGTGATTTGGTGTCTGCTCTCATGAGAGG 1457
Db 1473 AGAGCGGAAATTAGTTTAAACGAGGTTTAAATATGTTGGGTGGGCTGAGCTTATGAGAGG 1532
Qy 1458 TGCTGTATCTATGGCTTTTGCATACAAAGTTTAAAGGGGCGGGGACACAGATGTACG 1517
Db 1533 TGCCGTTTCTATGGCCCTTGCTTAAATCAGTTTACAGGGGAGGTCACTCAGTTAGG 1592
Qy 1518 CGGGAATGCAATCATGATCAAGATACGATTAACCTGTCTGTCTTTTGAACAGTGGTGT 1577
Db 1593 CGCAATATGCAATTAATGATCAAGTACTATCACTGTCTGTCTTTTTCAGCAGACAGTCTGT 1652
Qy 1578 TGGTATGCTGACCAACCACTCAT--AGCTACCTATTACCGCACCAAGCGCCACAC 1634
Db 1653 TGGGTGTGATGACCAAACTTTGATTAAGATATGTACCTTACCAACCAACTTGAAGCAG 1712
Qy 1635 GAGCATGTTATCTGATGACCAACACCCCAAAATCCATATATCCCTTTGTTGGACCAAGA 1694
Db 1713 AATGATCTTCTGAAACCAACGACCCCAAAATCCCTTCAATTTGTCACATCTTTCGACGAC 1772
Qy 1695 CTCGTTCAATGAGCCTTCAGGGAACCAATATGTGCTCGGCTGACAGTATACGTGGCTT 1754
```

```
Db 1773 ACAAGACTCAGAAGCTGATCTGGAAAGCCATGTATACCCGTCGCCACAGTTTGGGATGCT 1832
Qy 1755 CTTGACACGGCCCACTCGAAACCGTGCAATTAATCTACTGGAGACAATTTGATGACTCTCTTCAT 1814
Db 1833 CTTTCAACCCATCTCATACAGTGCATTAATCTGGAGAAAGTTTGAATGCAATTCAT 1892
Qy 1815 CGACCCCTCTTTGGAGGTCTGTGCTTTGTACCCCTTTGTTCCAGGTTCTTCAACTGA 1871
Db 1893 CGGTCCAGTTTTCGGTGGACGAGGTTTGTGTACCTTTGCTCAGGATCACCGACAGA 1949
```

RESULT 3

```
US-09-830-123-1
; Sequence 1, Application US/09830123
; Patent No. 6803500
; GENERAL INFORMATION:
; APPLICANT: Iida, Shigeru
; APPLICANT: Tanaka, Sachiko
; TITLE OF INVENTION: Inagaki, Yoshihide
; FILE REFERENCE: 001560-397
; CURRENT APPLICATION NUMBER: US/09/830.123
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: PCT/JP00/05722
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: JP 11/236800
; PRIOR FILING DATE: 1999-08-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2237
; TYPE: DNA
; ORGANISM: Ipomoea nil
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2237)
; OTHER INFORMATION: Nucleotide sequence of DNA encoding for protein regulating the
; OTHER INFORMATION: pH of vacuoles
US-09-830-123-1
```

```
Query Match 35.6%; Score 774.8; DB 4; Length 2237;
Best Local Similarity 69.2%; Pred. No. 1.3e-187;
Matches 1096; Conservative 0; Mismatches 467; Indels 21; Gaps 2;
```

```
Qy 319 TTATCGACATCTGATCAGCTTCTGTGTTGCGTTGGAATCTCTTTGTGCACTTCTTTGT 378
Db 339 TTGTTACGCTGATCATGCTTCCGTTGTGTGTAAGAACCTTTTGTGGCGTTGCTTGGC 398
Qy 379 GCTTGTATTTGTTCTTGTGTCATCTTTTGGAGAGAAATAGATGGAACGAATCCATCACC 438
Db 399 GCATGCATTTGTTCTTGGCCATCTACTCGAGGAGAAATCGCTGGGTGAACGAATCCATTA 458
Qy 439 GCTTGTGTGTTGGGTAGGCATGCGTGTACCAATTTTGTGATTTAGTAAAGGAAAAGC 498
Db 459 GCCCTTAATTTGTTTGTGACCGGAGTTGTAATTTTGTCTCTTAGCGGAGAAAGAGT 518
Qy 499 TCGCATCTTCTCGTCTTTAGTGAAGAGCTTTTCTTATATATCTTTTCCACCCCAATATA 558
Db 519 TCACATCTTCTCGTCTTTAGCGAAGATCTTTCTTATATATCTCTCTGCCACCTATAATA 578
Qy 559 TTCAATCAGGGTTTCAAGTAAAAAAGACAGATTTTTCGCAATTTTCGTGACTATTATG 618
Db 579 TTCAATCGGGTTTCAAGTAAAAAAGACAGATTTTTCGTTGAACTTCATGACAATTTATG 638
Qy 619 CTTTTTGGTGTGTGGGACTATTATTTCTTGTGCAATCATCTCTAGGTGTAAACAG 678
Db 639 CTGTTTGGAGCTATTGGCACACTTATTAGCTGTTCTATTATATCTTTTGGTGGCGTCAAA 698
Qy 679 TCTTTTAAAGAGTTGGACATTTGGAACCTTTTTCACCTTGGTGTGATTTCTTGTCTATTGGTCC 738
Db 699 ATTTTCAAGCACTTAGACATTTGACCTTTCTGGAATTTGGAGATTTATTAGCAATTTGGTGG 758
Qy 739 ATATTTGCTCAACAGAGATTCAAGTATGATGTAACACTGCGAGGTTTCTGAATCAAGACGACACCT 798
```

Db 759 ATATTGCTGCAACCGATCTGTTTGACATTTGCAAGTGTCTCAGTCAGATGAGACGCC 818
Qy 799 TTGCTTTACAGCTTTGTATTGCGAGAGGGTGTGTGAATGATGCAACCTCAGTTGTGGTC 858
Db 819 CTACTTTACAGTCTCGTGTGAGAGAGGGGTGCTCAATGATGCTACATCTGTGGTCTT 878
Qy 859 TTCAACGGGATTCAGAGCTTTGATCTCACTCACTCACTAAACCGAAGCTGCTTTTCATCTT 918
Db 879 TTTAATGCTATTCAAAGTTTTCGACATGACTAGTTTGTATCCAAAATTTGGGCTTCATTTTC 938
Qy 919 CTGGAACACTTCTGTTATTGTTTCTCCTAAGTACCTTGTGTTGGTGTGCAACCGTCTG 978
Db 939 ATTGGAACACTTCTGTTATTGTTTCTCGAGCACTTTTGGGCTGGGAATGGACTG 998
Qy 979 ATAACTGCTATGTTATCAAGAAGCTATATCTTTGGAAGCACTCAACTGACCGGAGGTT 1038
Db 999 TTTTGTGCTTATATTATCAAAAGCTATACCTTTGGCAGCACTCAACCGATCGTGAGGTT 1058
Qy 1039 GCCCTTATGATGCTTATGGCGTATCTTCTTATATGCTTGTGAGCTTTTCGACTTGAGC 1098
Db 1059 GCCCTTATGATGCTATGCTTCTACTTGTCTTATATAATGGCGAGTTATTCTCTAAGC 1118
Qy 1099 GGTATCTCTCACTGTGTTTCTGTGTTATGTGATGCTCCCATTCACATGGCACAATGTA 1158
Db 1119 GGCATACTACTGTATTCTCTGTGGAATGTGATGCTCATTTATACCTGSCACAATGTT 1178
Qy 1159 ACGGAGAGCTCAAGAATTAACAACAAGCATACCTTTGCACTTTGTCAATTTCTTGGGAG 1218
Db 1179 ACGGAGAGCTCAAGGGTCACTACTAGGCAATTCCTTTGCACTCTGTCAATTTGTGCGAG 1238
Qy 1219 ACATTTATTTCTTGTATGTTGGATGATGCTTGGACATGATGCAATGATGCAATGCGTG 1278
Db 1239 ACATTTATCTTCTCTATGTTGGTATGATGCTTGGATATCGAGAAATGGAAATTTGTG 1298
Qy 1279 AGTGACACACGGGAAACATCGATCCAGTGAGCTCAATCTAATGGGTCTGTCATGTTT 1338
Db 1299 AAAATAGTCAGGACTATCAGTTGCAGTGAGCTCAATATTGGTAGGCTTAATCTTAGTA 1358
Qy 1339 GGAAGAGAGCGGTTGCTTTCCGTTATGCTTTCTATCTAACTTAGCGCAAGAAGATCAA 1398
Db 1359 GGCAGAGCTGCGTTGCTATCCCTTGTGCTTTTATCCAACTTAGCAAGAAACTCT 1418
Qy 1399 AGCGAGAAATCACTTTAAATGACAGGTTGTGATTTGGTGTGCTGCTCATGAGGT 1458
Db 1419 TCGGACAAGATATCCTTTAGGCAAAATAAATTTGGTGGGCTTGAATGAGAGGC 1478
Qy 1459 GCTGTATCTATGGCTTTTGCTATACAAAGTTTACAGGGCGGSCACACAGATGTACGC 1518
Db 1479 GCGCTCTCAATAGCACTTGGTATATATAGTTTACACCTCGGGGCATACGTCATTTGCAC 1538
Qy 1519 GGAATGCAATCATGATCACGAGTACGATAAATCTGTCTGTTTTTTAGCACAGTGGTGT 1578
Db 1539 GAGAACGCAATAATGATTACAACTGTTACGGTTGTTCTGTTTTCAGCACAGTTGTATT 1598
Qy 1579 GGTATGCTGACCAACCACTCATAGCTTACCTATACCGCACAGAGCGCCACACAGGC 1638
Db 1599 GGGTTGATGACGAAGCCCTCATATAACCTTCTGCTACCCCGCACAGAGATGCCAAGC 1658
Qy 1639 -----ATGTTATCTGATGACAAACACCCCAAAATCCATACATATCCCTTTG 1693
Db 1659 GGTCAATCGTCAATGACAACTCCGACCCAGTAGTCGAGAGCACTTCACGGTGCACCTC 1718
Qy 1693 TTTGACCAA-----GACTGTTTCAATGAGCGCTTCAGGAAACCAATGTGCCCTCGGCT 1737
Db 1719 CTGACAAACCAACCTGACTCAGAAAGCGATATGATAACCGGACCTGAGGTGCTCGACCA 1778
Qy 1738 GACAGTATACGTGGCTTCTTGACACGGCCCACTCGAACCGTGCATTACTACTGAGACAA 1797
Db 1779 ACTGCTTGGCGATGCTGCTAAGGACGCCAACCCACACCGTGCACCGCTACTGCGGTAAG 1838
Qy 1798 TTTGATGACTCTTTCATCGCACCCGCTTTTGGAGGTGCTGCTTTGTACCCCTTTGTTCCA 1857

Db 1839 TTTGATGATTCGTTTATGCGTCCGTCGTTTGGCGGGCGGGATTCGTTCCGTTTGTGCG 1898
Qy 1858 GGTTCCTCAAAGTGAAGAAACCCCT 1881
Db 1899 GCGTCACAGTTGAGCAGAGCCCT 1922
RESULT 4
US-09-830-123-18
; Sequence 18, Application US/09830123
; Patent No. 6803500
; GENERAL INFORMATION:
; APPLICANT: Iida, Shigeru
; APPLICANT: Tanaka, Sachiko
; APPLICANT: Inagaki, Yoshihide
; TITLE OF INVENTION: Genes Encoding Proteins Regulating the pH of Vacuoles
; FILE REFERENCE: 001560-397
; CURRENT APPLICATION NUMBER: US/09/830,123
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: PCT/JP00/05722
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: JP 11/236800
; PRIOR FILING DATE: 1999-08-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 2361
; TYPE: DNA
; ORGANISM: Torenia hybrida
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(2361)
; OTHER INFORMATION: Nucleotide sequence of DNA encoding for protein regulating the pH of vacuoles
; OTHER INFORMATION: pH of vacuoles
US-09-830-123-18
Query Match 34.6%; Score 754.4; DB 4; Length 2361;
Best Local Similarity 68.4%; Pred. No. 2.2e-182;
Matches 1090; Conservative 0; Mismatches 471; Indels 33; Gaps 2;
Qy 319 TTATCGACATCTGATCAGCTTCTGTGTTGCGTTGAATCTCTTTGTTGCACTTCTTTGT 378
Db 444 TTGTGGAGCTCTGTCACGGTTCAGTGTGCTATACCTTATTTGTCACCTTCTCTGCG 503
Qy 379 GCTTGTATTGTTCTGTGTCATCTTTTGGAAAGATAGATGGATGAACGAATCATCAACC 438
Db 504 ACATGTATAGTATTGTCATCTCTCGAGGAAACCGTTGGATGAATCATCATTT 563
Qy 439 GCCTTGTATTGCTGGCTAGGCACTGGGTACCAATTTGTTGTTAGTAAAGGAAAGC 498
Db 564 GCCCTCAATTTGTTTAGCCACGGGAGTTATAATCTGTTAATAAGTGGTGGAAAGC 623
Qy 499 TCGCATCTTCTCGTCTTTAGTGAAGATCTTTTCTTATATATCTTTTGCACCACTTATA 558
Db 624 TCCATCTCTTGTGTTTTCAGTGAAGATCTTTTCTTATCTATGCGCTGCCACCAATCAT 683
Qy 559 TTCAATCGAGGTTTCAAGTAAAGAAAGAGAGGTTTTTCCGCAATTTTCGTCATTTATG 618
Db 684 TTTAATCGGGGTTCCAAAGTAAAGAAAGATCATTTCTTCGCAATTTTCGCAACTATAATG 743
Qy 619 CTTTTCGTCGCTGTGGGACTATTATTTCTTGACATCATATCTCTAGGTGTAACACAG 678
Db 744 ATGTTTGGAGAGTTGGTACTTGTATTCCTTATCATCATTTTCACTCGGTACAAATGCA 803
Qy 679 TTCTTTAAGAAAGTTGACATTTGGAAACCTTTTGA CTGGGTGATTATCTTGTCTATTGGTGCC 738
Db 804 TTCTTCCCAAAATGAACATGAGA---CTTGGAGTTGGAGATTATCTTCTATTGGAGCT 860
Qy 739 ATATTGCTGCAACAGATTCAGTATGTAACCTGAGGTTCTGAATCAAGACGAGACACT 798
Db 861 ATTTTCTGCAACAGACTCAGTTTGCATTTGCACTTACAGGTGCTAAGCCAGGACGAAACCA 920
Qy 799 TTGCTTTACAGTCTTGTATTTCGGAGAGGGTGTGTGAATGATGCAACGTCAGTTGTGCTC 858

Db	921	CTGTTTACAGCTCTAGTGTGTTGGCGAGGGTGTGTAANTCAGCGACTTCAGTGGTCTTA	980
Qy	859	TTGAACGCGATTCAGAGCTTTGATCTCACTCACCTAAACACCAAGCTGCTTTTCATCTTT	918
Db	981	TTTAAATGCAGTACAGAACTTCGACCTGCCCTCATATGCTACTGCTAAAGCTTCGAGCTT	1040
Qy	919	CTTGGAAACTTCTTGTAATTTGTTTCTCCTAAGTACCTTGTCTGGTGTCTGCAACGGTCTG	978
Db	1041	GTTTGGAAACTTCTTTTATTTATTTGCTTACAAGCACTGTCTGGGTGTCTTCTGACTGGATTG	1100
Qy	979	ATRAAGTCGTATGTTATCAAGAAGCTATACCTTTTGGAAAGGCACCTCAACTGACCCGAGGTT	1038
Db	1101	CTTAGTGCATACATCATAAAGAGCTCTATTTTGGAAAGGCACCTCCACTGATCGCAGGTT	1160
Qy	1039	GCCCTTATGATCTTATGGGCTATCTTTCTTATATGCTTCTGCTGAGCTTTTTCGACTTCGAGC	1098
Db	1161	GCATATGATACCTCATGGCTTATCTCTGTAATATGTTAGTCTGAAATTTTCGATTTTGAGC	1220
Qy	1099	GGTATCTCTACTGTGTTTCTGTGGTATTTGTGTATGTCCTCATACATAGCCACAATGTA	1158
Db	1221	GGTATCTCTACCGTGTCTTCTGTGGAAATTTGTATGTGCGACTATACATGGCAACAATGTC	1280
Qy	1159	ACGGAGAGCTCAAGAATAACAAACAAAGCATACCTTTTGCACATTTTGTCTTCTTGGGAG	1218
Db	1281	ACTGAAACATCAAGAGTTACACCAAGCATACATTTTCGCAATTTGCTTGTGTGTA	1340
Qy	1219	ACATTTATTTCTTGATGTTTGGAAATGGATGCGCTTGGACATTCACAAAGTGGAGATCCGTG	1278
Db	1341	ATATTTATATTTCTGTATGTTGGCATGATGCTTTAGACATTTGAGAAATGGAGATTCGTA	1400
Qy	1279	AGTGACACACCGGAAACATCGATCGAGTGAAGTCAATCTCTAAATGGGTCTGGTCACTGGTT	1338
Db	1401	AGCGCAGCATGACAAACATCTGCAGCTGTTCAGTGCACCTCTGTGGGATTTGTTTGTCTC	1460
Qy	1339	GGAAAGCAGGGTTCGCTTCTTCCGTTATCGTTTCTATCTAATCTTAGCCACAGAAATCAA	1398
Db	1461	TCAAGAGCAGCGCTTTGTAATTCCTTTTATCATTTCTCTCCAATCTGGGCCAAAAAGTCCCA	1520
Qy	1399	AGCGAGAAATCAACTTTTAAATCATCGAGTGTGTGATTTGGTGGTCTGTCTCATGAGAGGT	1458
Db	1521	CTCGAAAAATCAGTCTCAGCAGCAAAATATATATGTTGGGTGTCTTATGCGCGGA	1580
Qy	1459	GCTGTATCTATGGCTTTTGCATACAAAGTTTACAAGGGCCGGGCAACAGATGTACGC	1518
Db	1581	GCCTGTTCCATGGCTCTTGCTTACAAGAGTTTACTAGAGAGGTCTCAAGTGAACGT	1640
Qy	1519	GGGAATGCAATCATGATCAGAGTACGATTAATCTGTCTCTTTTATAGCAAGTGGTGT	1578
Db	1641	GAAAAATGCCATTTTCATCACAGTACAAATCACCAATTCCTTCTTCAGCACTGTGTGT	1700
Qy	1579	GGTATGCTGACCAACCACTCATAGCTACTTATACCGCACAGACGCCACCCAGCAGC	1638
Db	1701	GGTTTGATGACGAAGCCCTTCATCAATTTACTGTATCCCTCACAAAGCTTAAACAGATG	1760
Qy	1639	ATGTTATCTGATGACAAACACCCAAAAATCCATACATATCCCTTTTGTGGACCAAGACTCG	1698
Db	1761	GTCTCTTCAGAACCGTGACTCCAAATCTCATCAATCCCATCTTCGGGGAAAGTCAG	1820
Qy	1699	TTCAATGAGCCTTC-----AGGGAAACCAACAATGTG	1728
Db	1821	GACTCTGTGGCGCAACTATTTCAGCATCAGAGGTCAAACTTTCACAAGGTGGCGAAACCGTT	1880
Qy	1729	CCTCGGCTGACGATATACGTGGCTCTTTCAGACGGGCCCACTCGAACCGTGCATTACTAC	1788
Db	1881	GCTCGACCGGACGCGCTACGCATGTTACTCACAAAGCCCACTCATACGGTGCATATAT	1940
Qy	1789	TGGAGACAAATTTGATGACTCTCTCATGCGACCGCTCTTTGGAGTCTGTGCTTTGTACCC	1848
Db	1941	TGGAGAAAATTCGACAAATGCTTTTATGCGTCCGCTCTTTGGTGGCGTGGCTTTGTACCA	2000
Qy	1849	TTTGTTCAGGTTCTTCCAATCGAGAGAAACCCCTC	1882

```

Db      2001  TATGTTCCCGGTTCCACCGATGAACGAGCGTTC 2034

RESULT 5
US-09-800-729-22
; Sequence 22, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
;   APPLICANT:  N1 et al.
;   TITLE OF INVENTION:  32 Human secreted proteins
;   FILE REFERENCE:  P2044P1
;   CURRENT APPLICATION NUMBER:  US/09/800,729
;   CURRENT FILING DATE:  2001-03-08
;   PRIOR APPLICATION NUMBER:  PCT/US00/26013
;   PRIOR FILING DATE:  2000-09-22
;   PRIOR APPLICATION NUMBER:  60/155,709
;   PRIOR FILING DATE:  1999-09-24
;   NUMBER OF SEQ ID NOS:  217
;   SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 22
;   LENGTH:  1581
;   TYPE:  DNA
; ORGANISM:  Homo sapiens
; FEATURE:
;   NAME/KEY:  SITE
;   LOCATION:  (112)
; OTHER INFORMATION:  n equals a,t,g, or c
;   NAME/KEY:  SITE
;   LOCATION:  (959)
; OTHER INFORMATION:  n equals a,t,g, or c
;   NAME/KEY:  SITE
;   LOCATION:  (1565)
; OTHER INFORMATION:  n equals a,t,g, or c
US-09-800-729-22

```

Query Match 4.2%; Score 91.2; DB 4; Length 1581;
Best Local Similarity 47.6%; Pred. No. 3.8e-13;
Matches 369; Conservative 6; Mismatches 370; Indels 30

QY	522	AGATCTTTTCTTCATATATCTTTTGGCACCCATTAATTAATCAATGCAGGGTTTCAAGTAA	581
Db	433	AGAAAGTATTTTTTCAACATCTCTTCGCCCTCCAATTAATTTTTCATGCTGGATACAGCTTAAA	492
QY	582	AAAGAAGCAGTTTTTTCGCAATTTTCGNGACTATTATATGCTTTTTCGGTGCCTGTGGGACTAT	641
Db	493	GAAGAGACATTTTTTCAGAAATCTTGGATCTATTAATCTGGCCTATGCGCTTCTTGGGAGCTGC	552
QY	642	TATTTCTTGGCAATCATATCTCTAGGTGTAAACACAGTCTCTTTAAGAAGTTGGACATT--	699
Db	553	TGKTTCATGCTTCATTATTTGGAATCTCATGTATGGTGTGGTGAAGCTCATGAAGATTAT	612
QY	700	-----GGAACCTTTGACTTGGGTGATTAATCTTGTCTATTTGGTGCCATATTTCG	746
Db	613	GGGACAGCTCTCAGATAAAATTTTACTACAGAGATGKCTCTTTTTTGGAGCAATCATCTC	672
QY	747	TGCAACAGATTCAGTATGTACACTGCAGGTTCGAAATCAAGACGAGACACCTTGG--CT	803
Db	673	TGCCACTGACCCAGTGACTGTCTTGGCGATATTTAAATGAAATTGCATGCGACGTTGGATCT	732
QY	804	TTACAGTCTTGTATTTTCGGAGAGGGTGTGTGAATGATGCACACGTCAAGTTGTGGCTTTCAA	863
Db	733	TTACGCACTCTCTTTTGGAGAGACGCTCTAAATGATGCTGTGTGCCATTGKACTGKCTC	792
QY	864	CGCAATTCAGAGCTTTGATCTCACTCACTTAACACGAAAGCTGCTTTTCACTCTCTTGG	923
Db	793	GTCTATTGTGTGCCCTACCAGCAGCGGAGCTGAACACTCAGCCCTTTGATGCTGCTGCCTT	852
QY	924	AAACTCTTGTATTGTTTCTCCTAAAGTACCTTGGTGTGTCGCAACCGGCTCTGATAAG	983
Db	853	TTTTTAAGTCAGTTGGCATTTTCTAGGTATATTTAGTGGCTCTTTTACCATTGGGAGCTGT	912
QY	984	TGCGTATGTTA-----TCAGAAGCTATACTTTTGGAAGGCACCTCAACTGACCG	1031

Db	913	GACTGGTGTGTGACTGCTCAGTGA	CTAAGTTTACCAAAKGCACNGCTTCCCCCTGCT	972
Qy	1032	AGAGTTGCCCTTATGATGCTTATGCGGTATCTTTCTTATATGCTTGCTGAGCTTTTTCGA	1091	
Db	973	GGAGACGGCGCTGTTCTTCTCTCAITGCTCTGGAGCACGTTTCTCTTGGCAGAGCCTCGGG	1032	
Qy	1092	CTTGAGCGGTATCCTCACTGHTGTTTTTCTGTGGTATTGTGATGCCCATTTACACATGGCA	1151	
Db	1033	ATTTACAGGTGTGTGAGTCTGCTCTTTTCTGTGGAATCACACAAGCTCATTTACACCTACAA	1092	
Qy	1152	CAATGTAACGGAGAGCTCAAGAATAACAAACAAGCATACCTTTTGCAACTTTGTCTTCT	1211	
Db	1093	CAATCTGTCGGTGGAACTCAAGAGTCCAAACAGCAGCTCTTTTGAGGTGTTCATTTCT	1152	
Qy	1212	TGGCGAGACATTTATTTTCTTGATGTTGGAATGGATGCCCTTGGACATTCACAAG	1266	
Db	1153	GGCAGAGAACTTCATCTTCTCCTACATGGGCCTGGCACTGTTTACCTTCCAGAAG	1207	

RESULT 6

```

RES001.6
US-09-800-729-58
; Sequence 58, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 58
; LENGTH: 1354
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-800-729-58

```

Query Match	3.08;	Score 64.4;	DB 4;	Length 1354;
Best Local Similarity	54.7%;	Pred. No. 2.5e-06;		
Matches 128;	Conservative 0;	Mismatches 106;	Indels 0;	Gaps 0;
Qy 1033	GAGTTGCCCTTATGATGCTATGGCGTATCTTTCTTATATGCTTGCTGAGCTTTTCGAC	1092		
Db				
18	GAGACGGCGCTGTTCTCTCATGTCTCTGGAGACAGTTCTCTTGGCAGAGCGCTGGGA	77		
Qy 1093	TTGAGCGGTATCCTCATCTGTGTTTTCTGTGGTATTTGTGATGTCCTCATACATGGCAC	1152		
Db				
78	TTTACAGGTGTGTAGCTGTCTTTCTGTGGAAATCACACAAGCTATTACACCTACAAC	137		
Qy 1153	AATGTAACGGAGAGCTCAAGAATAACACAAGAAGCATACCTTTGCACTTTGTCTATTCTT	1212		
Db				
138	AACTGTGCGTGGAAATCAAGAGTCGAACCAAGCAGCTCTTTGAGTGTTTACATTTCCCTG	197		
Qy 1213	CGCGAGACATTTATTTTCTGTATGTTGGAAATGGAGCCCTTGGACATTTGACAAG	1266		
Db				
198	GCAGAGAACTTCATCTTCTCCTACATGGGCGCTGGCACTGTTTACCTTCCAGAAG	251		

RESULT 7

```

RES001 7
US-09-800-729-57
; Sequence 57, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIORITY APPLICATION NUMBER: PCT/US00/26013

```

```

; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 1688
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: SITE
; LOCATION: (21)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (69)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (99)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-800-729-57

Query Match      3.0%; Score 64.4; DB 4; Length 1688;
Best Local Similarity 54.7%; Pred. No. 2.7e-06;
Matches 128; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

Qy      1033 GAGGTGCGCTATGATGCTTATGGCGTATCTTTCTTATATGCTTGAGCCTTTTCGAC 1092
Db      345 GAGACGCGGTGTGTTCTTCCCTCATGCTCGGAGCAGCTTCTCTTGGCAGAACGCTGCGGA 404

Qy      1093 TTGAGCGGTATCCTCAGCTGTGTTTTCTGTGGTATTTGATGTGCCATTACACATGGCAC 1152
Db      405 TTTCACAGGTGTGTGAGTGTGCTCTTTCTGTGGAATCACACAAGCTCATTACACCTACAC 464

Qy      1153 AATGTAACGGAGAGCTCAAGAAATAACAACAAGCATACCTTTTGCAAATTGTGCAATTCCTT 1212
Db      465 AATCTGCGGTGGAAATCAAGAAATCGAATCGAATCGAAGCGCTCTTTGAGGTGTTACATTCCTG 524

Qy      1213 GCGGAGACATTTATTTTTCTTGATGTGGAAATGGATGCCCTTGGACATTTGACAAG 1266
Db      525 GCACAGAACTTCATCTTCTCTCATCGGCTGGCACTGTATTACCTTCCAGAAG 578

```

RESULT 8

```

US-09-949-016-849
; Sequence 849, Application US/09949016
; Patent NO. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 849
; LENGTH: 4452
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-849

```



```

; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 1291
; TYPE: DNA
; ORGANISM: Tribolium castaneum
US-09-524-101D-5

Query Match      2.5%; Score 53.8; DB 4; Length 1291;
Best Local Similarity 62.0%; Pred. No. 0.0012;
Matches 85; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy      2042  CATGGCCAACTTTGAACTGTTTGATGTATGTAATTAATTAATTCATAATTTGTTTGTGT 2101
         ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1129  CACGGCCGCTTTGATGATTAGTTATTTCTATTAATTAATTTTGTACTTTATGCAAT 1188

Qy      2102  AACACAAACTACACATTTGTTTATGTTTTCGAATTTGGTTTTGCTTCGAAAAAATAAAAA 2161
         ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1189  ATCCAGTTTACITTTGTTGTAATATTTTATTAATAAATTTCTACGTTTAAAAAATAAAAA 1248

Qy      2162  AAAAAAAAAAAAAAAA 2178
         ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1249  AAAAAAAAAAAAAAAA 1265
         ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 11
US-08-747-221B-36
; Sequence 36, Application US/08747221B
; Patent No. 6063610
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heeka Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80524
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747-221B
; FILING DATE: No. 6063610ember 12, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 11..1594
US-08-747-221B-36

```

Query Match 2.5%; Score 53.8; DB 3; Length 2007;

[illegible]

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999

```

	Query Match	2.5%	Score 53.8;	DB 3;	Length 2007;
	Best Local Similarity	52.4%;	Pred. No. 0.0015;		
	Matches 118;	Conservative 0;	Mismatches 107;	Indels 0;	Gaps 0;
Qy	1954	AAATTATGCTTTTGTGTAATATCCATTGTTGTAATATTGTTGGAGACAGAGAAATCTGT	2013		
Db	233	AACAAATTCGTTTTAGTGAATTTGGCGATTCAACAGATGGTGTACTGTGCTAATTTGT	174		
Qy	2014	CCTAACGTTTTGAGACAGAAAGCAAAACATGGCAACTTTTGAAGCTGTTTGAATGATGAT	2073		

Db 173 CCCTCTCTTGAAGAACTGAACATAAATGATTAATGAGCGCACATTATTTATATT 114
Qy 2074 GTAATTATATTCATATTTGTTTGTGTAACACAACTACACATTTGTTTATGTTTCAA 2133
Db 113 GATATATATACCATCTTTGTATCATATTTGCTTTTATTTTTCATTTTATTTATTTCA 54
Qy 2134 TTTGGTTTTCCTCGAAAAAATTTTATATATTTTATATTTTATTTTATTTTCA 2178
Db 53 AATATATTTGTTTAT 9

RESULT 13

US-09-005-051-36

; Sequence 36, Application US/09005051

; Patent No. 6291222

; GENERAL INFORMATION:

; APPLICANT: Silver, Gary W.

; APPLICANT: Wisniewski, Nancy

; TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid

; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carol Talkington Verser, Ph.D.

; ADDRESSEE: Heska Corporation

; STREET: 1825 Sharp Point Drive

; CITY: Fort Collins

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80525

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: WordPerfect for Windows, Version 7.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/005,051

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/747,221

; FILING DATE: No. 6291222ember 12, 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Verser, Carol Talkington

; REGISTRATION NUMBER: 37,459

; REFERENCE/DOCKET NUMBER: FC-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 970/493-7272

; TELEFAX: 970/484-9505

; INFORMATION FOR SEQ ID NO: 36:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2007 nucleotides

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 11..1594

US-09-005-051-36

Query Match 2.5%; Score 53.8; DB 3; Length 2007;

Best Local Similarity 52.4%; Pred. No. 0.0015;

Matches 118; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

Qy 1954 AAATATGCTTTTGTGTAATAATATCCATTTGTAATATTTGTTGTGAGACAGAAATCTGT 2013

Db 1775 AACAAATCTGTTTGTAGTATTTGCGCATTTCAACAGATGGTGTACTGTGCTTAAATTTGT 1834

Qy 2014 CCTAACGTTTGTGAGACAGAAAGCAACATGCGCACTTTGTAAGTGTGTTGATTCATGAT 2073

Db 1835 CGCTCTTCTTGAAGAACTGAACATAAATGATTAATGAGCGCACATTATTTATATTT 1894

Qy 2074 GTAATTATATTCATATTTGTTTGTGTAACAACTACACATTTGTTTATGTTTCAA 2133

Db 1895 GATATATATACCATCTTTGTATCATATTTGCTTTTATTTTTCATTTTATTTTCA 1954
Qy 2134 TTTGGTTTTCCTCGAAAAAATTTTATATATTTTATATTTTATTTTATTTTCA 2178
Db 1955 AATATATTTGTTTAT 1999

RESULT 14

US-09-005-051-38/c

; Sequence 38, Application US/09005051

; Patent No. 6291222

; GENERAL INFORMATION:

; APPLICANT: Silver, Gary W.

; APPLICANT: Wisniewski, Nancy

; TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid

; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carol Talkington Verser, Ph.D.

; ADDRESSEE: Heska Corporation

; STREET: 1825 Sharp Point Drive

; CITY: Fort Collins

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80525

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: WordPerfect for Windows, Version 7.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/005,051

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/747,221

; FILING DATE: No. 6291222ember 12, 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Verser, Carol Talkington

; REGISTRATION NUMBER: 37,459

; REFERENCE/DOCKET NUMBER: FC-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 970/493-7272

; TELEFAX: 970/484-9505

; INFORMATION FOR SEQ ID NO: 38:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2007 nucleotides

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-09-005-051-38

Query Match 2.5%; Score 53.8; DB 3; Length 2007;

Best Local Similarity 52.4%; Pred. No. 0.0015;

Matches 118; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

Qy 1954 AAATATGCTTTTGTGTAATAATATCCATTTGTAATATTTGTTGTGAGACAGAAATCTGT 2013

Db 233 AACAAATCTGTTTGTAGTATTTGCGCATTTCAACAGATGGTGTACTGTGCTTAAATTTGT 174

Qy 2014 CCTAACGTTTGTGAGACAGAAAGCAACATGCGCACTTTGTAAGTGTGTTGATTCATGAT 2073

Db 173 CGCTCTTCTTGAAGAACTGAACATAAATGATTAATGAGCGCACATTATTTATATTT 114

Qy 2074 GTAATTATATTCATATTTGTTTGTGTAACAACTACACATTTGTTTATGTTTCAA 2133

Db 113 GATATATATACCATCTTTGTATCATATTTGCTTTTATTTTTCATTTTATTTTCA 54

Qy 2134 TTTGGTTTTCCTCGAAAAAATTTTATATATTTTATATTTTATTTTATTTTCA 2178

Db 53 AATATATTTGTTTAT 9

